Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

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SIGNAL PEPTIDE
HUMAN -19 MQIELSTCFF LCLLRFCFS
PIG MÕLELSTCVF LCLLPLGFS
MOUSE MÕIALFACFF LSLFNFCSS
\*\* \* \* \* \* \* \* \* \*

# FIG. 1A

A1 DOM HUMAN PIG MOUSE		ATRRYYLGAV AIRRYYLGAV AIRRYYLGAV *******		LG-ELPVDAR LLRELHVDTR LLSVLHTDSR * * * *	FPPRVPKSFP FPATAPGALP FLPRMSTSFP *	FNTSVVYKKT LGPSVLYKKT FNTSIMYKKT * ****
	50	LFVEFTDHLF VFVEFTDQLF VFVEYKDQLF *** * **	NIAKPRPPWM SVARPRPPWM NIAKPRPPWM * *****	GLLGPTIQAE GLLGPTIQAE GLLGPTIWTE ******	VYDTVVITLK VYDTVVVTLK VHDTVVITLK * **** ***	
	100	AVGVSYWKAS AVGVSFWKSS AVGVSYWKAS **** *	EGAEYDDOTS EGAEYEDHTS EGDEYEDOTS ** *** **	QREKEDDKVF QREKEDDKVL QMEKEDDKVF * *****	PGGSHTYVWQ PGKSQTYVWQ PGESHTYVWQ ** * ****	VLKENGPMAS VLKENGPTAS VLKENGPMAS ******
	150	DPLCLTYSYL DPPCLTYSYL DPPCLTYSYM *******	SHVDLVKDLN	SGLIGALLVC SGLIGALLVC SGLIGALLVC ******	REGSLAKEKT REGSLTRERT KEGSLSKERT **** * *	QTLHKFILLF QNLHEFVLLF QMLYQFVLLF * * * ***
	200	AVFDEGKSWH AVFDEGKSWH AVFDEGKSWH ******	SARNDSWTŘA	RDAASARAWP MDPAPARAQP MDSASARDWP * * * * *	KMHTVNGYVN AMHTVNGYVN KMHTVNGYVN ******	RSLPGLIGCH RSLPGLIGCH RSLPGLIGCH ******
	250	RKSVYWHVIG KKSVYWHVIG RKSVYWHVIG ******	MGTTPEVHSI MGTSPEVHSI MGTTPEIHSI *** ** ***	FLEGHTFLVR FLEGHTFLVR FLEGHTFFVR ******	NHRQASLEIS HHRQASLEIS NHRQASLEIS ******** APC/IXa	PITFLTAOTL PLTFLTAOTF PITFLTAOTL *******
	300	LMDLGQFLLF LMDLGQFLLF LIDLGQFLLF * ******	CHISSHHHGG CHISSHKHDG ***** *	MEAYVKVDSC MEAHVRVESC MEAYVKVDSC *** * * **	PEEPOLRMKN AEEPOLRRKA PEESOWOKKN ** * *	NEEAEDYDDD DE-EEDYDDN NN-EEMEDYD * *
	350	LTDSEMDVVR LYDSDMDVVR DDLYSEMDMF	FDDDNSPSFI	QIR QIR QIR QIR ***		

FIG. 1B

A2 DOMA HUMAN PIG MOUSE	AIN 373	SVAKKHPKTW	VHYIAAEEED VHYISAEEED IHYISAEEED *** ****	WDYAPAVPSP		NNGPQRIGRK NSGPQRIGRK SNGPHRIGRK ** ****
	423		DETFKTREAI DVTFKTRKAI DETFKTRETI * **** *	QHESGLLGPL ***	LYGEVGDTLL LYGEVGDTLL LYGEVGDTLL ******	IIFKNQASRP IIFKNKASRP IIFKNQASRP ****
	473	YNIYPHGITD YNIYPHGITD YNIYPHGITD ******	A2 II VRPLYSRRLP VSALHPGRLL VSPLHARRLP * * **	WHIBITOR EPI KGVKHLKDFP KGWKHLKDMP RGIKHVKDLP ** ** **	ILPGEIFKYK ILPGETFKYK IHPGEIFKYK * *** *** F.IXa B	WTVTVEDGPT WTVTVEDGPT ******** INDING
	523	KSDPRCLTRY KSDPRCLTRY KSDPRCLTRY	YSSSINLEKD	LASGLIGPLL LASGLIGPLL LASGLIGPLL *******	APO ICYKESVDOR ICYKESVDOR ICYKESVDOR *******	<u>GNO</u> IMSDKRN GNOMMSDKRN
	573		RSWYLTENIQ QSWYLAENIQ QSWYITENMQ *** ** *	RFLPNPAGVQ RFLPNPDGLQ RFLPNAAKTQ *****	LEDPEFQASN PQDPEFQASN PQDPGFQASN ** ****	IMHSINGYVF IMHSINGYVF IMHSINGYVF *******
	623		EVAYWYILSI EVAYWYILSV EVAYWHILSV	GAQTDFLSVF GAQTDFLSVF GAQTDFLSIF *******	FSGYTFKHKM FSGYTFKHKM FSGYTFKHKM ******	VYEDTLTLFP VYEDTLTLFP ******
	673	FSGETVFMSM	ENPGLWVLGC	HNSDLRNRGM HNSDFRKRGM **** * ***	TALLKVSSCD TALLKVYSCD TALLKVSSCD ******	KNTGDYYEDS RDIGDYYDNT KSTSDYYEEI * ***
	723	↑ YEDISAYLLS YEDIPGFLLS YEDIPTQLVN ****		/APC		

FIG. 1C

B DOMAIN HUMAN 74 PIG MOUSE	SFAÖNSRPPS	TROKOFNATT ASOKOFOTIT TRKKKFKDST * * *	IPENDIEKTD SPEDDVE-LD IPKNDMEKIE * * **	PWFAHRTPMP PQSGERTQAL PQFEEIAEML *	KIQNVSSSDL EELSVPSGDG KVQSVSVSDM * *
79	1 LMLLRQS-PT SMLLGQN-PA LMLLGQSHPT *** *	PHGLSLSDLQ PHGSSSSDLQ PHGLFLSDGQ *** * *	EAKYETFSDD EARNEADD EAIYEAIHDD ** * **	PSPGAIDSNN YLPGARERNT HSPNAIDSNE * * *	SLSEMTHFRP APSAAARLRP GPSKVTQLRP * **
84	O QLHHSGDMVF ELHHSAERVL ESHHSEKIVF ***	TPEP	NEKLGTTAAT EK NKSLETTIEV	ELKKLDFKVS ELKKLDSKMS KWKKLGLQVS ***	ST-SNNLIS- SSSDLLKTSP SLPSNLMTT- *
88	8 TIPSDNLAAG TIPSDTLSAE TILSDNLKAT	T ERTHSLGPPF	I PQVNFRSQLO	3 AIVLGKNSSF	P LTESGGPLSL H FIGAGVPLGS G LVGSHVPLNA **
93	TEED	ESGLMNSQESHES DSTLMYSQES **	SWGKNVSSTE SLGENVSPVE LPRDNILSIE * *	SGRLFKGKRA SDGIFEKERA NDRLLREKRF *	
98	9 ALFKVSISLL VLFKVNISLV TLFKDNVSLM *** **		TNRKTHIDGP TNRKIHIDDA TNEKLHTESP ** * *	SLLIENSPSV ALLTENRAS- TSIENSTTDL	WQNILESDTE QDAILKVNSE
103	9 FKKVTPLIHD  IQEVTALIHD * **	ATFMDKNTTA	LRLNHMSNKT SGLNHVSN LRLNHMLNRT *** *	TSSKNMEMVQ  TSTKNKDIFH	QKKEGPIPPD RKDEDPIPQD
108		MLFLPESARWW MLFLSESSNW *	IKGPLGKNPL	SSERGPSPEL	LTSSGSGKSV
113	KGÕSSGQGRI	KVVVGKGEFT RVAVEEEELS KVTVEQDGFT * *	KGKEMML	PSSRNLFLTN PNSELTFLTN PHNMSIFLTT * ***	SADVQGNDTH
118	9 NQEKKIQEEI SÕGKKSREEM NÕEKNIQEEI *	EKKETLIQEN ERREKLVÕEK EK-EALIEEK * * *	VVLPQIHTVT VDLPQVYTAT VVLPQVHEAT * ***	GTKNFLRNIF	LLSTRONVEG HOSTEPSVEG ILGTRONI
123	9 SYDGAYAPVL FDGGSHAPVP SLYEVHVPVL **	QDFRSLNDST QDSRSLNDSA QNITSINNST * * * *	NRTKKHTAHF ERAETHIAHF NTVQIHMEHF * **	SAIREEAP	LEAPGNRT

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1287	IVEKYACTTR MVKNYP	ISPNTSQONF GPGPRSA SQKNI	VTQRSKRALK VPRRVKQSLK TTQRSKRALG	QFRLPLEETE QIRLPLEEIK QFRL	LEKRIIVDDT PERGVVLNAT
1337	STQWSKNMKH STRWS STQWLKTINC			QSPLSDCLTR  KSSLSDS-SV	
1387				PAASYR  QASSYIYDFK	
1433	HFLQGAKKNN PILQGAKRNN NFLKETKINN * * **	LSLAILTLEM LSLPFLTLEM PSLAILPWNM ** * *	TGDOREVGSL AGGOGKISAL FIDOGKFTSP	GTSATNSVTY GKSAAGPLAS GKSNTNSVTY * *	GKLEKAVLSS
1483	PDLPKTSGKV AGLSEASGKA PTLPEESGKI ***	EFLPKVRVHŘ			GSLLQGTEGA EIFLQKTRGP EVFLQKIQGP ***
1533	IKWNEANRPG VNLNKVNRPG TKWNKAKRHG * * *	KVPFLRVATE  ESIKGKTES-	SSAKTPSKLL RTPSKLL -SKNTRSKLL * ****		TQIPKEEWKS PPMPKE-WES AQIPKDMWKS * * *
1583	QEKSPEKTAF LEKSPKSTAL KEKSPEIISI ****	RTKDIISLPL	D RHESNHSIA R PHGNSHSIG		R EAAWTKÕGGP
1633	ERLCSONPPY GRLCAPKPPV QRTCSQIPPV * * * * * *	LRRHÕR			

# FIG. 1D-2

FIG. 1E

					1	
A3 DON	NIAN				••	
HUMAN PIG MOUSE	1690	SFQKKTRHYF SFQKRTRHYF SVQQKTRHYF * * ****	IAAVERLWDY IAAVEQLWDY IAAVERLWDY ****	GMSSSPHVLR GMSESPRALR GMSTS-HVLR *** * **	A Xa NRAQSGSVPQ NRAQNGEVPR NRYQSDNVPQ ** * **	FKKVVFQEFT FKKVVFREFA FKKVVFQEFT *****
	1740	DGSFTOPLYR DGSFTOPSYR DGSFSOPLYR **** **	GELNKHLGLL	GPYIRAEVED GPYIRAEVED GPYIRAEVED ***********************************	NIMVTFRNQA NIMVTFKNQA NIMVTFKNQA ************************************	SRPYSFYSSL
	1790	ISYEEDOROG ISYPDDÖEQG ISYKEDQR-G *** **	AEPRKNFVKP AEPRHNFVQP EEPRRNFVKP *** *** *	NETKTYFWKV NETRTYFWKV NETKIYFWKV ***	OHHMAPTKDE OHHMAPTEDE OHHMAPTEDE *******	FDCKAWAYFS FDCKAWAYFS FDCKAWAYFS ******
	1840	DVDLEKDVHS DVDLEKDVHS DVDLERDMHS **** * **	GLIGPLLICR	TNTLNPAHGR ANTLNAAHGR ANTLNPAHGR ****	QVTVQEFALF QVTVQEFALF QVSVQEFALL ** *****	FTIFDETKSW FTIFDETKSW FTIFDETKSW ******
	1890	YFTENMERNC YFTENVERNC YFTENVKRNC ****	RAPCNIOMED RAPCHLOMED KTPCNFOMED ** ***	PTFKENYRFH PTLKENYRFH PTLKENYRFH ** *****	AINGYIMDTL AINGYVMDTL AINGYVMDTL ******	PGLVMAQDQR PGLVMAQNQR PGLVMAQDQR ******
	1940	IRWYLLSMGS IRWYLLSMGS IRWYLLSMGN *******	NENIHSIHFS NENIQSIHFS ****	GHVFTVRKKE GHVFSVRKKE GHVFTVRKKE **** ****	EYKMALYNLY EYKMAVYNLY EYKMAVYNLY *****	PGVFETVEML PGVFETVEML PGVFETLEMI *****
	1990	PSKAGIWRVE PSKVGIWRIE PSRAGIWRVE ** ****		MSTLFLVYSN MSTTFLVYSK MSTLFLVYSK *** *****	<i>J</i>	

FIG. 1F

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C1 DOMAIN HUMAN 2020 PIG MOUSE	KCQTPLGMAS ECQAPLGMAS QCQIPLGMAS ** *****	GHIRDFQITA GRIRDFQITA GSIRDFQITA * ******	SGOYGOWAPK	LARLHYSGST	NAWSTKDPHS
2070	WIKVDLLAPM WIKVDLLAPM WIKVDLLAPM ******	IIHGIKTOGA IIHGIMTÕGA IVHGIKTÕGA * *** ***	ROKESSLYTS	OFTIMYSLDG	RNWOSYRGNS
2120	TGTLMVFFGN TGTLMVFFGN TGTLMVFFGN ******	VDSSGIKHNI VDASGIKHNI VDSSGIKHNS ** *****	FNPPIIARYI FNPPIVARYI FNPPIIARYI ****	RLHPTHYSIR	STLRMELMGCDLN STLRMELMGCDLN STLRMELMGCDLN *******

# FIG. 1G

RPQ RPR
RPQ * *
QWT
RWT
TWH **
RME
RLE
RLE * *

FIG. 1H

Inventor(s): Lollar Application No: To be Assigned Atty Dkt No: 007157/276516

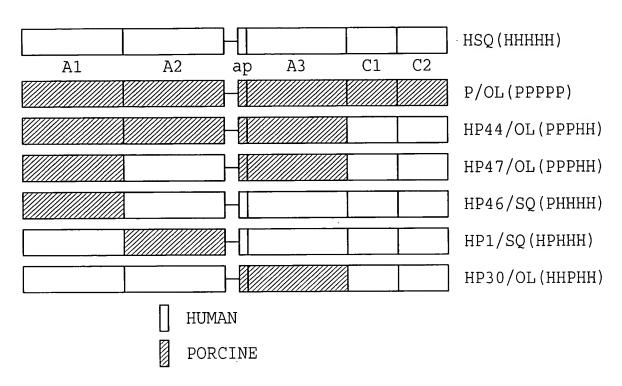


FIG. 2

Application No: To be Assigned Atty Dkt No: 007157/276516

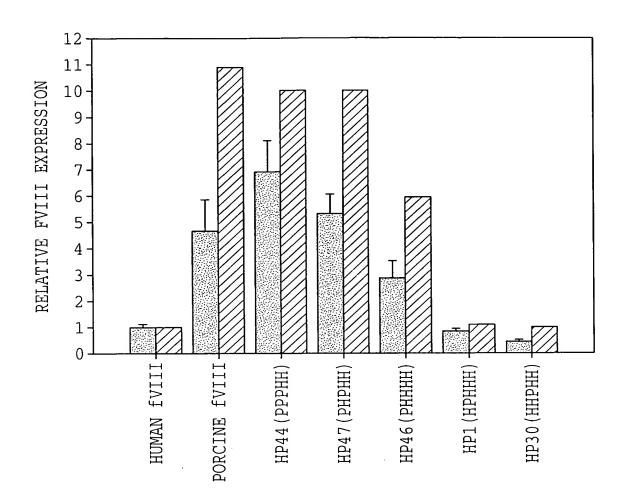


FIG. 3

Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

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#### AMINO ACID SEQUENCE OF HP44/OL

```
1
      MOLELSTCVF LCLLPLGFSA
                              IRRYYLGAVE
                                         LSWDYROSEL LRELHVDTRF
  51
      PATAPGALPL
                  GPSVLYKKTV
                              FVEFTDQLFS
                                          VARPRPPWMG
                                                      LLGPTIOAEV
101
      YDTVVVTLKN
                 MASHPVSLHA
                              VGVSFWKSSE
                                          GAEYEDHTSO
                                                      REKEDDKVLP
151
      GKSQTYVWQV
                  LKENGPTASD
                              PPCLTYSYLS
                                          HVDLVKDLNS
                                                      GLIGALLVCR
                              VFDEGKSWHS
                                          ARNDSWTRAM
 201
      EGSLTRERTQ
                  NLHEFVLLFA
                                                     DPAPARAQPA
 251
      MHTVNGYVNR
                  SLPGLIGCHK
                              KSVYWHVIGM
                                          GTSPEVHSIF
                                                      LEGHTFLVRH
                              MDLGQFLLFC
 301
      HRQASLEISP
                  LTFLTAOTFL
                                         HISSHHHGGM
                                                      EAHVRVESCA
 351
      EEPOLRRKAD
                  EEEDYDDNLY
                              DSDMDVVRLD
                                          GDDVSPFIQI
                                                      RSVAKKHPKT
401
      WVHŶISAEEE
                  DWDYAPAVPS
                              PSDRSYKSLY
                                          LNSGPQRIGR
                                                      KYKKARFVAY
451
501
                  IPYESGILGP
                              LLYGEVGDTL
                                          LIIFKÑKASR
      TDVTFKTRKA
                                                      PYNIYPHGIT
                  LKGWKHLKDM
                              PILPGETFKY
                                          KWTVTVEDGP
                                                      TKSDPRCLTR
      DVSALHPGRL
 551
      YYSSSINLEK
                  DLASGLIGPL LICYKESVDO
                                          RGNOMMSDKR
                                                      NVILFSVFDE
 601
                              QPQDPEFQAS
      NOSWYLAENI
                  QRFLPNPDGL
                                          NIMHSINGYV
                                                      FDSLOLSVCL
                              FFSGYTFKHK
                                                      PFSGETVFMS
 651
      HEVAYWYILS
                  VGAQTDFLSV
                                          MVYEDTLTLF
                  CHNSDLRNRG
                                          DRDIGDYYDN
                                                      TYEDIPGFLL
 701
                              MTALLKVYSC
      MENPGLWVLG
 751
                  FAONSRPPSA
                              SAPKPPVLRR
                                          HORDISLPTF
                                                      QPEEDKMDYD
      SGKNVIEPRS
                              ODPRSFOKRT
 801
      DIFSTETKGE
                  DFDIYGEDEN
                                          RHYFIAAVEQ
                                                      LWDYGMSESP
 851
                              REFADGSFTO
      RALRNRAQNG
                  EVPRFKKVVF
                                          PSYRGELNKH
                                                      LGLLGPYIRA
 901
      EVEDNIMVTF
                  KNQASRPYSF
                              YSSLISYPDD
                                          QEQGAEPRHN
                                                      FVQPNETRTY
 951
                  TEÕEFDCKAW
                                                      LICRANTLNA
                              AWFSDVDLEK
                                          DVHSGLIGPL
      FWKVQHHMAP
1001
                              TKSWYFTENV
      AHGRQVTVQE
                  FALFFTIFDE
                                          ERNCRAPCHL
                                                      QMEDPTLKEN
                                                      IHFSGHVFSV
1051
      YRFHAINGYV
                  MDTLPGLVMA
                              ONORIRWYLL
                                          SMGSNENIHS
                              VEMLPSKVGI
1101
                  YNLYPGVFET
                                          WRIECLIGEH
                                                      LOAGMSTTFL
      RKKEEYKMAV
1151
1201
      VYSKKCQTPL
                  GMASGHIRDF
                              QITASGQYGQ
                                          WAPKLARLHY
                                                      SGSINAWSTK
      EPFSWIÑVDL
                              TOGAROŘFSŠ
                                          LYISOFIIMY
                                                      SLDGKKWQTY
                  LAPMIIHGIK
                                          ARYIRLHPTH
                                                      YSIRSTLRME
1251
      RGNSTGTLMV
                  FFGNVDSSGI
                              KHNIFNPPII
1301
      LMGCDLNSCS
                  MPLGMESKAI
                              SDAQITASSY
                                          FTNMFATWSP
                                                      SKARLHLQGR
                              KTMKVTGVTT
1351
      SNAWRPOVNN
                  PKEWLQVDFQ
                                          OGVKSLLTSM
                                                      YVKEFLISSS
1401
      QDGHQWTLFF
                  QNGKVKVFQG NQDSFTPVVN
                                          SLDPPLLTRY
                                                      LRIHPQSWVH
1451
                  ČEAODLY*
      OIALRMEVLG
```

1-19 SIGNAL PEPTIDE 20-391 A1 DOMAIN 392-759 A2 DOMAIN 760-783 OL LINKER 784-1154 ap-A3 1155-1307 C1 DOMAIN 1308-1467 C2 DOMAIN

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# HP44/OL NUCLEOTIDE SEQUENCE

1	<u> አጥርርአርርጥአር</u>	AGCTCTCCAC	CTGTGTCTTT	CTGTGTCTCT	TGCCACTCGG
1					
	TACGTCGATC	TCGAGAGGTG	GACACAGAAA	GACACAGAGA	ACGGTGAGCC
51	CTTTAGTGCC	ATCAGGAGAT	ACTACCTGGG	CGCAGTGGAA	CTGTCCTGGG
	GAAATCACGG	TAGTCCTCTA	TGATGGACCC	GCGTCACCTT	GACAGGACCC
101					
101	ACTACCGGCA	AAGTGAACTC	CTCCGTGAGC	TGCACGTGGA	CACCAGATTT
	TGATGGCCGT	TTCACTTGAG	GAGGCACTCG	ACGTGCACCT	GTGGTCTAAA
151					
151	CCTGCTACAG	CGCCAGGAGC	TCTTCCGTTG	GGCCCGTCAG	TCCTGTACAA
	GGACGATGTC	GCGGTCCTCG	AGAAGGCAAC	CCGGGCAGTC	AGGACATGTT
201	AAAGACTGTG	TTCGTAGAGT	TCACGGATCA	ACTTTTCAGC	GTTGCCAGGC
201					
		AAGCATCTCA	AGTGCCTAGT	TGAAAAGTCG	CAACGGTCCG
251	CCAGGCCACC	ATGGATGGGT	CTGCTGGGTC	CTACCATCCA	GGCTGAGGTT
	GGTCCGGTGG	TACCTACCCA			
2.2.4			GACGACCCAG	GATGGTAGGT	CCGACTCCAA
301	TACGACACGG	TGGTCGTTAC	CCTGAAGAAC	ATGGCTTCTC	ATCCCGTTAG
	ATGCTGTGCC	ACCAGCAATG	GGACTTCTTG	TACCGAAGAG	TAGGGCAATC
251					
351	TCTTCACGCT	GTCGGCGTCT	CCTTCTGGAA	ATCTTCCGAA	GGCGCTGAAT
	AGAAGTGCGA	CAGCCGCAGA	GGAAGACCTT	TAGAAGGCTT	CCGCGACTTA
401	ATGAGGATCA	CACCAGCCAA	AGGGAGAAGG	AAGACGATAA	AGTCCTTCCC
101					
	TACTCCTAGT	GTGGTCGGTT	TCCCTCTTCC	TTCTGCTATT	TCAGGAAGGG
451	GGTAAAAGCC	AAACCTACGT	CTGGCAGGTC	CTGAAAGAAA	ATGGTCCAAC
	CCATTTTCGG	TTTGGATGCA	CACCGTCCAG	GACTTTCTTT	TACCAGGTTG
E 0 1					
501	AGCCTCTGAC	CCACCATGTC	TTACCTACTC	ATACCTGTCT	CACGTGGACC
	TCGGAGACTG	GGTGGTACAG	AATGGATGAG	TATGGACAGA	GTGCACCTGG
551	TGGTGAAAGA	CCTGAATTCG	GGCCTCATTG	GAGCCCTGCT	GGTTTGTAGA
221					
	ACCACTTTCT	GGACTTAAGC	CCGGAGTAAC	CTCGGGACGA	CCAAACATCT
601	GAAGGGAGTC	TGACCAGAGA	AAGGACCCAG	AACCTGCACG	AATTTGTACT
001		ACTGGTCTCT			
	CTTCCCTCAG		TTCCTGGGTC	TTGGACGTGC	TTAAACATGA
651	ACTTTTTGCT	GTCTTTGATG	AAGGGAAAAG	TTGGCACTCA	GCAAGAAATG
	TGAAAAACGA	CAGAAACTAC	TTCCCTTTTC	AACCGTGAGT	CGTTCTTTAC
701					
701	ACTCCTGGAC	ACGGGCCATG	GATCCCGCAC	CTGCCAGGGC	CCAGCCTGCA
	TGAGGACCTG	TGCCCGGTAC	CTAGGGCGTG	GACGGTCCCG	GGTCGGACGT
751	ATGCACACAG	TCAATGGCTA	TGTCAACAGG	TCTCTGCCAG	GTCTGATCGG
, , ,					
	TACGTGTGTC	AGTTACCGAT	ACAGTTGTCC	AGAGACGGTC	CAGACTAGCC
801	ATGTCATAAG	AAATCAGTCT	ACTGGCACGT	GATTGGAATG	GGCACCAGCC
	TACAGTATTC	TTTAGTCAGA	TGACCGTGCA	CTAACCTTAC	CCGTGGTCGG
0.51					
851	CGGAAGTGCA	CTCCATTTTT	CTTGAAGGCC	ACACGTTTCT	CGTGAGGCAC
	GCCTTCACGT	GAGGTAAAAA	GAACTTCCGG	TGTGCAAAGA	GCACTCCGTG
901	CATCGCCAGG	CTTCCTTGGA	GATCTCGCCA	CTAACTTTCC	TCACTGCTCA
701					
	GTAGCGGTCC	GAAGGAACCT	CTAGAGCGGT	GATTGAAAGG	AGTGACGAGT
951	GACATTCCTG	ATGGACCTTG	GCCAGTTCCT	ACTGTTTTGT	CATATCTCTT
	CTGTAAGGAC		CGGTCAAGGA	TGACAAAACA	GTATAGAGAA
1001					
1001	CCCACCACCA	TGGTGGCATG	GAGGCTCACG	TCAGAGTAGA	
	GGGTGGTGGT	ACCACCGTAC	CTCCGAGTGC	AGTCTCATCT	TTCGACGCGG
1051	GAGGAGCCCC	ACCTCCCCAC	GAAAGCTGAT	GAAGAGGAAG	ATTATGATGA
1031					
	CTCCTCGGGG		CTTTCGACTA	CTTCTCCTTC	TAATACTACT
1101	CAATTTGTAC	GACTCGGACA	TGGACGTGGT	CCGGCTCGAT	GGTGACGACG
	GTTAAACATG		ACCTGCACCA	GGCCGAGCTA	
1153					
1151	TGTCTCCCTT		CGCTCGGTTG	CCAAGAAGCA	
	ACAGAGGGAA	ATAGGTTTAG	GCGAGCCAAC	GGTTCTTCGT	AGGGTTTTGG
1201		ACATCTCTGC	AGAGGAGGAG	GACTGGGACT	ACGCCCCCCC
1201					
	ACCCACGTGA		TCTCCTCCTC	CTGACCCTGA	TGCGGGGGCG
1251	GGTCCCCAGC	CCCAGTGACA	GAAGTTATAA	AAGTCTCTAC	TTGAACAGTG
	CCAGGGGTCG	GGGTCACTGT	CGGCAATATT	TTCAGAGATG	AACTTGTCAC
1201					
1301			AAATACAAAA	AAGCTCGATT	CGTCGCTTAC
	CAGGAGTCGC	TTAACCATCC	TTTATGTTTT	TTCGAGCTAA	GCAGCGAATG
	<del>_</del>				

	-8-	- 44	(no		
1351	ACGGATGTAA TGCCTACATT		'33 TCGTAAAGCT AGCATTTCGA	ATTCCGTATG TAAGGCATAC	AATCAGGAAT TTAGTCCTTA
1401	CCTGGGACCT	TTACTTTATG	GAGAAGTTGG	AGACACACTT	TTGATTATAT
	GGACCCTGGA	AATGAAATAC	CTCTTCAACC	TCTGTGTGAA	AACTAATATA
1451	TTAAGAATAA	AGCGAGCCGA	CCATATAACA	TCTACCCTCA	TGGAATCACT
	AATTCTTATT	TCGCTCGGCT	GGTATATTGT	AGATGGGAGT	ACCTTAGTGA
1501	GATGTCAGCG	CTTTGCACCC	AGGGAGACTT	CTAAAAGGTT	GGAAACATTT
	CTACAGTCGC	GAAACGTGGG	TCCCTCTGAA	GATTTTCCAA	CCTTTGTAAA
1551	GAAAGACATG	CCAATTCTGC	CAGGAGAGAC	TTTCAAGTAT	AAATGGACAG
	CTTTCTGTAC	GGTTAAGACG	GTCCTCTCTG	AAAGTTCATA	TTTACCTGTC
1601	TGACTGTGGA	AGATGGGCCA	ACCAAGTCCG	ATCCTCGGTG	CCTGACCCGC
	ACTGACACCT	TCTACCCGGT	TGGTTCAGGC	TAGGAGCCAC	GGACTGGGCG
1651	TACTACTCGA	GCTCCATTAA	TCTAGAGAAA	GATCTGGCTT	CGGGACTCAT
	ATGATGAGCT	CGAGGTAATT	AGATCTCTTT	CTAGACCGAA	GCCCTGAGTA
1701	TGGCCCTCTC	CTCATCTGCT	ACAAAGAATC	TGTAGACCAA	AGAGGAAACC
	ACCGGGAGAG	GAGTAGACGA	TGTTTCTTAG	ACATCTGGTT	TCTCCTTTGG
1751	AGATGATGTC	AGACAAGAGA	AACGTCATCC	TGTTTTCTGT	ATTCGATGAG
	TCTACTACAG	TCTGTTCTCT	TTGCAGTAGG	ACAAAAGACA	TAAGCTACTC
1801	AATCAAAGCT	GGTACCTCGC	AGAGAATATT	CAGCGCTTCC	TCCCCAATCC
	TTAGTTTCGA	CCATGGAGCG	TCTCTTATAA	GTCGCGAAGG	AGGGGTTAGG
1851	GGATGGATTA	CAGCCCCAGG	ATCCAGAGTT	CCAAGCTTCT	AACATCATGC
	CCTACCTAAT	GTCGGGGTCC	TAGGTCTCAA	GGTTCGAAGA	TTGTAGTACG
1901	ACAGCATCAA	TGGCTATGTT	TTTGATAGCT	TGCAGCTGTC	GGTTTGTTTG
	TGTCGTAGTT	ACCGATACAA	AAACTATCGA	ACGTCGACAG	CCAAACAAAC
1951	CACGAGGTGG	CATACTGGTA	CATTCTAAGT	GTTGGAGCAC	AGACGGACTT
	GTGCTCCACC	GTATGACCAT	GTAAGATTCA	CAACCTCGTG	TCTGCCTGAA
2001	CCTCTCCGTC	TTCTTCTCTG	GCTACACCTT	CAAACACAAA	ATGGTCTATG
	GGAGAGGCAG	AAGAAGAGAC	CGATGTGGAA	GTTTGTGTTT	TACCAGATAC
2051	AAGACACACT	CACCCTGTTC	CCCTTCTCAG	GAGAAACGGT	CTTCATGTCA
	TTCTGTGTGA	GTGGGACAAG	GGGAAGAGTC	CTCTTTGCCA	GAAGTACAGT
2101	ATGGAAAACC	CAGGTCTCTG	GGTCCTTGGG	TGCCACAACT	CAGACTTGCG
	TACCTTTTGG	GTCCAGAGAC	CCAGGAACCC	ACGGTGTTGA	GTCTGAACGC
2151	GAACAGAGGG	ATGACAGCCT	TACTGAAGGT	GTATAGTTGT	GACAGGGACA
	CTTGTCTCCC	TACTGTCGGA	ATGACTTCCA	CATATCAACA	CTGTCCCTGT
2201	TTGGTGATTA	TTATGACAAC	ACTTATGAAG	ATATTCCAGG	CTTCTTGCTG
	AACCACTAAT	AATACTGTTG	TGAATACTTC	TATAAGGTCC	GAAGAACGAC
2251	AGTGGAAAGA TCACCTTTCT	ATGTCATTGA TACAGTAACT	ACCTAGGAGC		ATTCAAGACC
2301	CCCTAGTGCG GGGATCACGC	AGCGCTCCAA TCGCGAGGTT	AGCCTCCGGT TCGGAGGCCA	CCTGCGACGG	CATCAGAGGG GTAGTCTCCC
2351	ACATAAGCCT	TCCTACTTTT	CAGCCGGAGG	AAGACAAAAT	GGACTATGAT
	TGTATTCGGA	AGGATGAAAA	GTCGGCCTCC.	TTCTGTTTTA	CCTGATACTA
2401	GATATCTTCT CTATAGAAGA	CAACTGAAAC GTTGACTTTG	GAAGGGAGAA CTTCCCTCTT		TTTACGGTGA AAATGCCACT
2451	GGATGAAAAT	CAGGACCCTC	GCAGCTTTCA	GAAGAGAACC	CGACACTATT
	CCTACTTTTA	GTCCTGGGAG	CGTCGAAAGT	CTTCTCTTGG	GCTGTGATAA
2501	TCATTGCTGC	GGTGGAGCAG	CTCTGGGATT	ACGGGATGAG	CGAATCCCCC
	AGTAACGACG	CCACCTCGTC	GAGACCCTAA	TGCCCTACTC	GCTTAGGGGG
2551	CGGGCGCTAA	GAAACAGGGC	TCAGAACGGA	GAGGTGCCTC	GGTTCAAGAA
	GCCCGCGATT	CTTTGTCCCG	AGTCTTGCCT	CTCCACGGAG	CCAAGTTCTT
2601	GGTGGTCTTC	CGGGAATTTG	CTGACGGCTC	CTTCACGCAG	CCGTCGTACC
	CCACCAGAAG	GCCCTTAAAC	GACTGCCGAG	GAAGTGCGTC	GGCAGCATGG
2651	GCGGGGAACT	CAACAAACAC	TTGGGGCTCT	TGGGACCCTA	CATCAGAGCG
	CGCCCCTTGA	GTTGTTTGTG	AACCCCGAGA	ACCCTGGGAT	GTAGTCTCGC
2701	GAAGTTGAAG	ACAACATCAT	GGTAACTTTC	AAAAACCAGG	CGTCTCGTCC
	CTTCAACTTC	TGTTGTAGTA	CCATTGAAAG	TTTTTTGGTCC	GCAGAGCAGG
2751	CTATTCCTTC	TACTCGAGCC FIG	TTATTTCTTA		CAGGAGCAAG

Inventor(s): Lollar Application No: To be Assigned Atty Dkt No: 007157/276516

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		121			
	GATAAGGAAG	ATGAGCTCGG		AGGCCTACTA	
2801	GGGCAGAACC	TCGACACAAC	TTCGTCCAGC	CAAATGAAAC	CAGAACTTAC
2001	CCCGTCTTGG	AGCTGTGTTG	AAGCAGGTCG	GTTTACTTTG	GTCTTGAATG
2851	TTTTGGAAAG	TGCAGCATCA	CATGGCACCC	ACAGAAGACG	AGTTTGACTG
702T					
	AAAACCTTTC	ACGTCGTAGT	GTACCGTGGG	TGTCTTCTGC	TCAAACTGAC
2901	CAAAGCCTGG	GCCTACTTTT	CTGATGTTGA	CCTGGAAAAA	GATGTGCACT
	GTTTCGGACC	CGGATGAAAA	GACTACAACT	GGACCTTTTT	CTACACGTGA
2951	CAGGCTTGAT	CGGCCCCCTT	CTGATCTGCC	GCGCCAACAC	CCTGAACGCT
2751	GTCCGAACTA	GCCGGGGGAA	GACTAGACGG	CGCGGTTGTG	GGACTTGCGA
2001					TTTTCACTAT
3001	GCTCACGGTA	GACAAGTGAC	CGTGCAAGAA	TTTGCTCTGT	
	CGAGTGCCAT	CTGTTCACTG	GCACGTTCTT	AAACGAGACA	AAAAGTGATA
3051	TTTTGATGAG	ACAAAGAGCT	GGTACTTCAC	TGAAAATGTG	GAAAGGAACT
	AAAACTACTC	TGTTTCTCGA	CCATGAAGTG	ACTTTTACAC	CTTTCCTTGA
3101	GCCGGGCCCC	CTGCCATCTG	CAGATGGAGG	ACCCCACTCT	GAAAGAAAAC
2101	CGGCCCGGGG	GACGGTAGAC	GTCTACCTCC	TGGGGTGAGA	CTTTCTTTTG
2151					
3151	TATCGCTTCC	ATGCAATCAA	TGGCTATGTG	ATGGATACAC	TCCCTGGCTT
	ATAGCGAAGG	TACGTTAGTT	ACCGATACAC	TACCTATGTG	AGGGACCGAA
3201	AGTAATGGCT	CAGAATCAAA	GGATCCGATG	GTATCTGCTC	AGCATGGGCA
	TCATTACCGA	GTCTTAGTTT	CCTAGGCTAC	CATAGACGAG	TCGTACCCGT
3251	GCAATGAAAA	TATCCATTCG	ATTCATTTTA	GCGGACACGT	GTTCAGTGTA
2221					
	CGTTACTTTT	ATAGGTAAGC	TAAGTAAAAT	CGCCTGTGCA	CAAGTCACAT
3301	CGGAAAAAGG	AGGAGTATAA	AATGGCCGTG	TACAATCTCT	ATCCGGGTGT
	GCCTTTTTCC	TCCTCATATT	TTACCGGCAC	ATGTTAGAGA	TAGGCCCACA
3351	CTTTGAGACA	GTGGAAATGC	TACCGTCCAA	AGTTGGAATT	TGGCGAATAG
J J J I	GAAACTCTGT	CACCTTTACG	ATGGCAGGTT	TCAACCTTAA	ACCGCTTATC
3401	AATGCCTGAT	TGGCGAGCAC	CTGCAAGCTG	GGATGAGCAC	GACTTTCCTG
3401					
	TTACGGACTA	ACCGCTCGTG	GACGTTCGAC	CCTACTCGTG	CTGAAAGGAC
3451	GTGTACAGCA	AGAAGTGTCA	GACTCCCCTG	GGAATGGCTT	CTGGACACAT
	CACATGTCGT	TCTTCACAGT	CTGAGGGGAC	CCTTACCGAA	GACCTGTGTA
3501	TAGAGATTTT	CAGATTACAG	CTTCAGGACA	ATATGGACAG	TGGGCCCCAA
J J U I	ATCTCTAAAA	GTCTAATGTC	GAAGTCCTGT	TATACCTGTC	ACCCGGGGTT
3551	AGCTGGCCAG	ACTTCATTAT	TCCGGATCAA	TCAATGCCTG	GAGCACCAAG
3221					
	TCGACCGGTC	TGAAGTAATA	AGGCCTAGTT	AGTTACGGAC	CTCGTGGTTC
3601	GAGCCCTTTT	CTTGGATCAA	GGTGGATCTG	TTGGCACCAA	TGATTATTCA
	CTCGGGAAAA	GAACCTAGTT	CCACCTAGAC	AACCGTGGTT	ACTAATAAGT
3651	CGGCATCAAG	ACCCAGGGTG	CCCGTCAGAA	GTTCTCCAGC	CTCTACATCT
3031	GCCGTAGTTC	TGGGTCCCAC	GGGCAGTCTT	CAAGAGGTCG	GAGATGTAGA
3701	CTCAGTTTAT	CATCATGTAT	AGTCTTGATG	GGAAGAAGTG	GCAGACTTAT
3/01					
	GAGTCAAATA	GTAGTACATA	TCAGAACTAC	CCTTCTTCAC	CGTCTGAATA
3751		CCACTGGAAC			
		GGTGACCTTG		AAGAAACCGT	
3801	ATCTGGGATA	AAACACAATA	TTTTTAACCC	TCCAATTATT	GCTCGATACA
	TAGACCCTAT	TTTGTGTTAT	AAAAATTGGG	AGGTTAATAA	CGAGCTATGT
3851	TCCGTTTGCA		TATAGCATTC	GCAGCACTCT	TCGCATGGAG
2021				CGTCGTCAGA	
2001	AGGCAAACGT	GGGTTGAGTA	ATATCGTAAG		
3901	TTGATGGGCT	GTGATTTAAA	TAGTTGCAGC	ATGCCATTGG	GAATGGAGAG
	AACTACCCGA	CACTAAATTT	ATCAACGTCG	TACGGTAACC	CTTACCTCTC
3951	TAAAGCAATA	TCAGATGCAC	AGATTACTGC	TTCATCCTAC	TTTACCAATA
3331	ATTTCGTTAT	AGTCTACGTG	TCTAATGACG	AAGTAGGATG	AAATGGTTAT
4001	TGTTTGCCAC		TCAAAAGCTC	GACTTCACCT	CCAAGGGAGG
4001	1G111GCCHC				
		GACCAGAGGA			GGTTCCCTCC
4051		GGAGACCTCA		CCAAAAGAGT	
	TCATTACGGA	CCTCTGGAGT	CCACTTATTA	GGTTTTCTCA	CCGACGTTCA
4101		AAGACAATGA		AGTAACTACT	CAGGGAGTAA
1101	CCTGAAGGTC		TTCAGTGTCC	TCATTGATGA	
4151	AATCTCTGCT	TACCAGCATG	TATGTGAAGG	AGTTCCTCAT	CTCCAGCAGT
4 T D T					
	TAGAGACGA	ATGGTCGTAC		TCAAGGAGTA	GAGGTCGTCA

FIG. 5C

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4201				CAGAATGGCA GTCTTACCGT	
4251	TTTTCAGGGA	AATCAAGACT	CCTTCACACC		TCTCTAGACC
4301	CACCGTTACT	GACTCGCTAC	CTTCGAATTC	ACCCCCAGAG TGGGGGTCTC	TTGGGTGCAC
4351	CAGATTGCCC	TGAGGATGGA	GGTTCTGGGC	TGCGAGGCAC	AGGACCTCTA
4401	C G	ACTCCTACCT	CCAAGACCCG	ACGCTCCGTG	ICCIGGAGAI

1-57 SIGNAL PEPTIDE 58-1173 A1 DOMAIN 1174-2277 A2 DOMAIN 2278-2349 OL LINKER 2350-3462 ap-A3 DOMAINS 3463-3921 C1 DOMAIN 3922-4401 C2 DOMAIN

FIG. 5D

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#### AMINO ACID SEQUENCE OF HP46/SQ

```
MOLELSTCVF LCLLPLGFSA
                              IRRYYLGAVE
                                          LSWDYRQSEL
                                                      LRELHVDTRF
 51
                              FVEFTDOLFS
                                          VARPRPPWMG
      PATAPGALPL
                  GPSVLYKKTV
                                                      LLGPTIQAEV
101
                              VGVSFWKSSE
                                          GAEYEDHTSQ
                                                      REKEDDKVLP
      YDTVVVTLKN
                  MASHPVSLHA
                                          HVDLVKDLNŠ
151
      GKSQTYVWQV
                  LKENGPTASD
                              PPCLTYSYLS
                                                      GLIGALLVCR
201
      EGSLTRERTO
                  NLHEFVLLFA
                              VFDEGKSWHS
                                          ARNDSWTRAM
                                                      DPAPARAOPA
251
                              KSVYWHVIGM
                                          GTSPEVHSIF
                                                      LEGHTFLVRH
      MHTVNGYVNR
                  SLPGLIGCHK
301
      HROASLEISP
                  LTFLTAQTFL
                              MDLGQFLLFC
                                          HISSHHHGGM
                                                      EAHVRVESCA
351
                  EEEDYDDNLY
                              DSDMDVVRLD
                                          GDDVSPFIQI
      EEPQLRRKAD
                                                      RSVAKKHPKT
401
                              PDDRSYKSOY
                                          LNNGPORIGR
                                                      KYKKVRFMAY
      WVHYIAAEEE
                  DWDYAPLVLA
                  IOHESGILGP
                              LLYGEVGDTL
                                          LIIFKNOASR
451
      TDETFKTREA
                                                      PYNIYPHGIT
501
      DVRPLYSRRL
                  PKGVKHLKDF
                              PILPGEIFKY
                                          KWTVTVEDGP
                                                      TKSDPRCLTR
551
      YYSSFVNMER
                  DLASGLIGPL
                              LICYKESVDQ
                                          RGNQIMSDKR
                                                      NVILFSVFDE
                              OLEDPEFOAŠ
FFSGYTFKHK
                  QRFLPNPAGV
601
      NRSWYLTENI
                                          NIMĤSINGYV
                                                      FDSLQLSVCL
      HEVAYWYILS
                                          MVYEDTLTLF
                                                      PFSGĒTVFMS
651
                   GAQTDFLSV
701
      MENPGLWILG
                  CHNSFLRNRG
                              MTALLKVSSC
                                          DKNTGDYYED
                                                      SYEDISAYLL
 751
      SKNNAIEPRS
                  FSONPPVLKR
                              HOREITRTTL
                                          OSDOEEIDYD
                                                      DTISVEMKKE
                                          LWDYGMSSSP
                                                      HVLRNRAOSG
801
      DFDIYDEDEN
                  OSPRSFOKKT
                              RHYFIAAVER
851
                  ÕEFTDGŜFTO
                                                      EVEDNIMVTF
      SVPOFKKVVF
                              PLYRGELNEH
                                          LGLLGPYIRA
901
      RNQASRPYSF
                  ŶSSLISYEEĎ
                                          FVKPNETKTY
                                                      FWKVQHHMAP
                              QRQGAEPRKN
                                                      AHGRÕVTVQE
      TKÕEFDCKAW
                  AYFSDVDLEK
 951
                              DVHSGLIGPL
                                          LVCHTNTLNP
                              ERNCRAPCNI
                                                      YRFHAINGYI
1001
                                          OMEDPTFKEN
      FALFFTIFDE
                  TKSWYFTENM
1051
      MDTLPGLVMA
                  ODORIRWYLL
                              SMGSNENIHS
                                          IHFSGHVFTV
                                                      RKKEEYKMAL
      YNLYPGVFET
1101
                  VEMLPSKAGI
                              WRVECLIGEH
                                          LHAGMSTLFL
                                                      VYSNKCQTPL
                  QITASGQYGQ
TQGARQKFSS
                                                      EPFSWIKVDL
1151
      GMASGHIRDF
                              WAPKLARLHY
                                          SGSINAWSTK
                                                      RGNSTGTLMV
1201
      LAPMIIHGIK
                              LYISQFIIMY
                                          SLDGKKWQTY
1251
      FFGNVDSSGI
                  KHNIFNPPII
                              ARYIRLHPTH
                                          YSIRSTLRME
                                                      LMGCDLNSCS
                  SDAOITASSY
                              FTNMFATWSP
                                          SKARLHLQGR
                                                      SNAWRPQVNN
1301
      MPLGMESKAI
                  KTMŘVTGVTT
                              QGVKSLLTSM
                                          YVKEFLISSS
                                                      QDGHQWTLFF
1351
      PKEWLOVDFO
      QNGKVŘVFQĜ
                              SLDPPLLTRY LRIHPOSWVH
1401
                  NODSFTPVVN
                                                      QIALRMEVLG
1451
      CEAODLY*
```

1-19 SIGNAL PEPTIDE 20-391 A1 DOMAIN 392-759 A2 DOMAIN 760-773 SQ LINKER 774-1144 ap-A3 1145-1297 C1 DOMAIN 1298-1457 C2 DOMAIN

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# HP46/SQ NUCLEOTIDE SEQUENCE

1	ATGCAGCTAG	AGCTCTCCAC	CTGTGTCTTT	CTGTGTCTCT	TGCCACTCGG
	TACGTCGATC	TCGAGAGGTG	GACACAGAAA	GACACAGAGA	
51	CTTTAGTGCC	ATCAGGAGAT TAGTCCTCTA	ACTACCTGGG TGATGGACCC	CGCAGTGGAA GCGTCACCTT	CTGTCCTGGG GACAGGACCC
101	GAAATCACGG ACTACCGGCA		CTCCGTGAGC	TGCACGTGGA	CACCAGATTT
101	TGATGGCCGT	TTCACTTGAG	GAGGCACTCG	ACGTGCACCT	GTGGTCTAAA
151	CCTGCTACAG	CGCCAGGAGC	TCTTCCGTTG	GGCCCGTCAG	TCCTGTACAA
	GGACGATGTC	GCGGTCCTCG	AGAAGGCAAC	CCGGGCAGTC	AGGACATGTT
201	AAAGACTGTG	TTCGTAGAGT	TCACGGATCA	ACTTTTCAGC	GTTGCCAGGC
251	TTTCTGACAC CCAGGCCACC	AAGCATCTCA ATGGATGGGT	AGTGCCTAGT CTGCTGGGTC	TGAAAAGTCG CTACCATCCA	CAACGGTCCG GGCTGAGGTT
251	GGTCCGGTGG	TACCTACCCA	GACGACCCAG	GATGGTAGGT	CCGACTCCAA
301	TACGACACGG	TGGTCGTTAC	CCTGAAGAAC	ATGGCTTCTC	ATCCCGTTAG
	ATGCTGTGCC	ACCAGCAATG	GGACTTCTTG	TACCGAAGAG	TAGGGCAATC
351	TCTTCACGCT	GTCGGCGTCT	CCTTCTGGAA	ATCTTCCGAA	GGCGCTGAAT
401	AGAAGTGCGA		GGAAGACCTT	TAGAAGGCTT	CCGCGACTTA
401	ATGAGGATCA TACTCCTAGT	CACCAGCCAA GTGGTCGGTT	AGGGAGAAGG TCCCTCTTCC	AAGACGATAA TTCTGCTATT	AGTCCTTCCC TCAGGAAGGG
451	GGTAAAAGCC	AAACCTACGT	CTGGCAGGTC	CTGAAAGAAA	ATGGTCCAAC
431	CCATTTTCGG	TTTGGATGCA	GACCGTCCAG	GACTTTCTTT	TACCAGGTTG
501	AGCCTCTGAC	CCACCATGTC	TTACCTACTC	ATACCTGTCT	CACGTGGACC
	TCGGAGACTG	GGTGGTACAG	AATGGATGAG	TATGGACAGA	GTGCACCTGG
551	TGGTGAAAGA	CCTGAATTCG	GGCCTCATTG	GAGCCCTGCT	GGTTTGTAGA
601	ACCACTTTCT	GGACTTAAGC	CCGGAGTAAC	CTCGGGACGA	CCAAACATCT
601	GAAGGGAGTC CTTCCCTCAG	TGACCAGAGA ACTGGTCTCT	AAGGACCCAG TTCCTGGGTC	AACCTGCACG TTGGACGTGC	AATTTGTACT TTAAACATGA
651	ACTTTTTGCT	GTCTTTGATG	AAGGGAAAAG	TTGGCACTCA	GCAAGAAATG
0.51	TGAAAAACGA	CAGAAACTAC	TTCCCTTTTC	AACCGTGAGT	CGTTCTTTAC
701	ACTCCTGGAC	ACGGGCCATG	GATCCCGCAC	CTGCCAGGGC	CCAGCCTGCA
	TGAGGACCTG	TGCCCGGTAC	CTAGGGCGTG	GACGGTCCCG	GGTCGGACGT
751	ATGCACACAG	TCAATGGCTA	TGTCAACAGG	TCTCTGCCAG	GTCTGATCGG
2.24	TACGTGTGTC	AGTTACCGAT	ACAGTTGTCC	AGAGACGGTC	CAGACTAGCC
801	ATGTCATAAG	AAATCAGTCT	ACTGGCACGT	GATTGGAATG CTAACCTTAC	GGCACCAGCC CCGTGGTCGG
851	TACAGTATTC CGGAAGTGCA	TTTAGTCAGA CTCCATTTTT	TGACCGTGCA CTTGAAGGCC	ACACGTTTCT	CGTGAGGCAC
031	GCCTTCACGT	GAGGTAAAAA	GAACTTCCGG	TGTGCAAAGA	GCACTCCGTG
901	CATCGCCAGG	CTTCCTTGGA	GATCTCGCCA	CTAACTTTCC	TCACTGCTCA
	GTAGCGGTCC	GAAGGAACCT	CTAGAGCGGT	GATTGAAAGG	AGTGACGAGT
951	GACATTCCTG	ATGGACCTTG	GCCAGTTCCT	ACTGTTTTGT	CATATCTCTT
1001		TACCTGGAAC		TGACAAAACA	
1001		TGGTGGCATG ACCACCGTAC	GAGGCTCACG CTCCGAGTGC	AGTCTCATCT	AAGCTGCGCC
1051		AGCTGCGGAG		GAAGAGGAAG	· - <del>-</del>
1031	CTCCTCGGGG			CTTCTCCTTC	
1101	CAATTTGTAC	GACTCGGACA	TGGACGTGGT	CCGGCTCGAT	GGTGACGACG
	GTTAAACATG			GGCCGAGCTA	
1151	TGTCTCCCTT		CGCTCAGTTG	CCAAGAAGCA	
1201		ATAGGTTTAG	GCGAGTCAAC		AGGATTTTGA ATGCTCCCTT
1201	IGGGIACATT	ACATTGCTGC	TGAAGAGGAG	GACIGGGACI	MIGCICCCII

1251	ACCCATGTAA AGTCCTCGCC	TGTAACGACG CCCGATGACA	ACTTCTCCTC GAAGTTATAA	CTGACCCTGA AAGTCAATAT	TACGAGGGAA TTGAACAATG
1301	TCAGGAGCGG GCCCTCAGCG	GGGCTACTGT GATTGGTAGG	CTTCAATATT	TTCAGTTATA AAGTCCGATT	AACTTGTTAC TATGGCATAC
1351	CGGGAGTCGC ACAGATGAAA	CTAACCATCC CCTTTAAGAC	TTCATGTTTT GCGTGAAGCT	TTCAGGCTAA ATTCAGCATG	ATACCGTATG AATCAGGAAT
1401	TGTCTACTTT CTTGGGACCT GAACCCTGGA	GGAAATTCTG TTACTTTATG AATGAAATAC	CGCACTTCGA GGGAAGTTGG CCCTTCAACC	TAAGTCGTAC AGACACACTG TCTGTGTGAC	TTAGTCCTTA TTGATTATAT AACTAATATA
1451	TTAAGAATCA AATTCTTAGT	AGCAAGCAGA TCGTTCGTCT	CCATATAACA GGTATATTGT	TCTACCCTCA AGATGGGAGT	CGGAATCACT GCCTTAGTGA
1501	GATGTCCGTC CTACAGGCAG	CTTTGTATTC GAAACATAAG	AAGGAGATTA TTCCTCTAAT	CCAAAAGGTG GGTTTTCCAC	TAAAACATTT ATTTTGTAAA
1551	GAAGGATTTT CTTCCTAAAA	CCAATTCTGC GGTTAAGACG	CAGGAGAAAT GTCCTCTTTA	ATTCAAATAT TAAGTTTATA	AAATGGACAG TTTACCTGTC
1601	TGACTGTAGA ACTGACATCT	AGATGGGCCA TCTACCCGGT	ACTAAATCAG TGATTTAGTC	ATCCGCGGTG TAGGCGCCAC	CCTGACCCGC GGACTGGGCG
1651	TATTACTCTA ATAATGAGAT	GTTTCGTTAA CAAAGCAATT	TATGGAGAGA ATACCTCTCT	GATCTAGCTT CTAGATCGAA	CAGGACTCAT GTCCTGAGTA
1701	TGGCCCTCTC ACCGGGAGAG	CTCATCTGCT GAGTAGACGA	ACAAAGAATC TGTTTCTTAG	TGTAGTCCAA ACATCTAGTT	AGAGGAAACC TCTCCTTTGG
1751	AGATAATGTC TCTATTACAG	AGACAAGAGG TCTGTTCTCC	AATGTCATCC TTACAGTAGG	TGTTTTCTGT ACAAAAGACA	ATTTGATGAG TAAACTACTC
1801	AACCGAAGCT TTGGCTTCGA	GGTACCTCAC CCATGGAGTG	AGAGAATATA TCTCTTATAT	CAACGCTTTC GTTGCGAAAG	TCCCCAATCC AGGGGTTAGG
1851	AGCTGGAGTA TCGACCTCAC	CAGCTTGAGG GTCGAACTCC	ATCCAGAGTT TAGGTCTCAA	CCAAGCCTCC GGTTCGAAGG	AACATCATGC TTGTAGTACG
1901	ACAGCATCAA TGTCGTAGTT	TGGCTATGTT ACCGATACAA	TTTGATAGTT AAACTATCAA	TGCAGTTGTC ACGTCAACAG	AGTTTGTTTG TCAAACAAAC AGACTGACTT
1951	CATGAGGTGG GTACTCCACC	CATACTGGTA GTATGACCAT	CATTCTAAGC GTAAGATTCG	ATTGGAGCAC TAACCTCGTG CAAACACAAA	TCTGACTGAA ATGGTCTATG
2001	CCTTTCTGTC GGAAAGACAG	TTCTTCTCTG AAGAAGAGAC	GATATACCTT CTATATGGAA	GTTTGTGTTT GAGAAACTGT	TACCAGATAC CTTCATGTCG
2051	AAGACACACT TTCTGTGTGA	CACCCTATTC GTGGGATAAG CAGGTCTATG	CCATTCTCAG GGTAAGAGTC GATTCTGGGG	CTCTTTGACA TGCCACAACT	GAAGTACAGC CAGACTTTCG
2101 2151	ATGGAAAACC TACCTTTTGG GAACAGAGGC	GTCCAGATAC ATGACCGCCT	CTAAGACCCC TACTGAAGGT	ACGGTGTTGA TTCTAGTTGT	GTCTGAAAGC GACAAGAACA
2201		TACTGGCGGA			~-~~~~~~
2251	GACCACTAAT	AATGCTCCTG ATGCCATTGA	TCAATACTTC ACCTAGGAGC	TATAAAGTCG TTCTCTCAGA	TATGAACGAC ATCCACCAGT
2301	TCATTTTTGT CTTGAAACGC	TACGGTAACT		AAGAGAGTCT TACTACTCTT	TAGGTGGTCA CAGTCAGATC
2351		GTAGTTGCCC	TTTATTGAGC GATACCATAT	ATGATGAGAA CAGTTGAAAT	GTCAGTCTAG GAAGAAGGAA
2401	TTCTCCTTTA	ACTGATACTA TTTATGATGA	CTATGGTATA	GTCAACTTTA	CTTCTTCCTT GCAGCTTTCA
2451		AAATACTACT	CCTACTTTTA		CGTCGAAAGT CTCTGGGATT
2501	TTTCTTTTGT ATGGGATGAG	GCTGTGATAA	AATAACGACG CATGTTCTAA	TCACCTCTCC	GAGACCCTAA TCAGAGTGGC
		,			

2551	TACCCTACTC AGTGTCCCTC	ATCGAGGGGT AGTTCAAGAA	GTACAAGATT AGTTGTTTTC	CTTTGTCCCG CAGGAATTTA	AGTCTCAGCG CTGATGGCTC
	TCACAGGGAG	TCAAGTTCTT	TCAACAAAAG	GTCCTTAAAT	GACTACCGAG
2601	CTTTACTCAG GAAATGAGTC	CCCTTATACC GGGAATATGG	GTGGAGAACT CACCTCTTGA	AAATGAACAT TTTACTTGTA	TTGGGACTCC AACCCTGAGG
2651	TGGGGCCATA ACCCCGGTAT	TATAAGAGCA ATATTCTCGT	GAAGTTGAAG CTTCAACTTC	ATAATATCAT TATTATAGTA	GGTAACTTTC CCATTGAAAG
2701	AGAAATCAGG TCTTTAGTCC	CCTCTCGTCC GGAGAGCAGG	CTATTCCTTC GATAAGGAAG	TATTCTAGCC ATAAGATCGG	TTATTTCTTA AATAAAGAAT
2751	TGAGGAAGAT ACTCCTTCTA	CAGAGGCAAG GTCTCCGTTC	GAGCAGAACC CTCGTCTTGG	TAGAAAAAAC ATCTTTTTTG	TTTGTCAAGC AAACAGTTCG
2801	CTAATGAAAC	CAAAACTTAC GTTTTGAATG	TTTTGGAAAG AAAACCTTTC	TGCAACATCA ACGTTGTAGT	TATGGCACCC ATACCGTGGG
2851	GATTACTTTG ACTAAAGATG	AGTTTGACTG	CAAAGCCTGG	GCTTATTTCT CGAATAAAGA	CTGATGTTGA GACTACAACT
2901	TGATTTCTAC CCTGGAAAAA	TCAAACTGAC GATGTGCACT	GTTTCGGACC CAGGCCTGAT	TGGACCCCTT	CTGGTCTGCC GACCAGACGG
2951	GGACCTTTTT ACACTAACAC	CTACACGTGA ACTGAACCCT	GTCCGGACTA GCTCATGGGA	ACCTGGGGAA GACAAGTGAC	AGTACAGGAA
3001	TGTGATTGTG TTTGCTCTGT	TGACTTGGGA TTTTCACCAT	CGAGTACCCT CTTTGATGAG	CTGTTCACTG ACCAAAAGCT	TCATGTCATT GGTACTTCAC
3051	AAACGAGACA TGAAAATATG	AAAAGTGGTA GAAAGAAACT	GAAACTACTC GCAGGGCTCC	TGGTTTTCGA CTGCAATATC	CCATGAAGTG CAGATGGAAG
3101	ACTTTTATAC ATCCCACTTT	CTTTCTTTGA TAAAGAGAAT	CGTCCCGAGG TATCGCTTCC	GACGTTATAG ATGCAATCAA	GTCTACCTTC TGGCTACATA
3151	TAGGGTGAAA ATGGATACAC	ATTTCTCTTA TACCTGGCTT	ATAGCGAAGG AGTAATGGCT	TACGTTAGTT CAGGATCAAA	ACCGATGTAT GGATTCGATG
3201	TACCTATGTG GTATCTGCTC	ATGGACCGAA AGCATGGGCA	TCATTACCGA GCAATGAAAA	GTCCTAGTTT CATCCATTCT	CCTAAGCTAC ATTCATTTCA
3251	CATAGACGAG GTGGACATGT	TCGTACCCGT GTTCACTGTA	CGTTACTTTT CGAAAAAAAAG	GTAGGTAAGA AGGAGTATAA	TAAGTAAAGT AATGGCACTG
3301	CACCTGTACA TACAATCTCT	CAAGTGACAT ATCCAGGTGT	GCTTTTTTTC TTTTGAGACA	TCCTCATATT GTGGAAATGT	TTACCGTGAC TACCATCCAA
	ATGTTAGAGA	TAGGTCCACA	AAAACTCTGT	CACCTTTACA TGGCGAGCAT	ATGGTAGGTT CTACATGCTG
3351	AGCTGGAATT TCGACCTTAA	TGGCGGGTGG ACCGCCCACC	AATGCCTTAT TTACGGAATA	ACCGCTCGTA	GATGTACGAC
3401	GGATGAGCAC CCTACTCGTG	ACTTTTTCTG TGAAAAAGAC	GTGTACAGCA CACATGTCGT	ATAAGTGTCA TATTCACAGT	GACTCCCCTG CTGAGGGGAC
3451		CTGGACACAT GACCTGTGTA	TAGAGATTTT ATCTCTAAAA	CAGATTACAG GTCTAATGTC	CTTCAGGACA GAAGTCCTGT
3501	ATATGGACAG TATACCTGTC	TGGGCCCCAA ACCCGGGGTT	AGCTGGCCAG TCGACCGGTC	ACTTCATTAT TGAAGTAATA	
3551	TCAATGCCTG AGTTACGGAC		GAGCCCTTTT CTCGGGAAAA	CTTGGATCAA GAACCTAGTT	GGTGGATCTG CCACCTAGAC
3601	TTGGCACCAA AACCGTGGTT	TGATTATTCA	CGGCATCAAG GCCGTAGTTC	ACCCAGGGTG TGGGTCCCAC	CCCGTCAGAA GGGCAGTCTT
3651	GTTCTCCAGC		CTCAGTTTAT		AGTCTTGATG
3701		GCAGACTTAT		CCACTGGAAC	CTTAATGGTC
3751	TTCTTTGGCA	ATGTGGATTC	ATCTGGGATA TAGACCCTAT	AAACACAATA	
3801	AAGAAACCGT TCCAATTATT				

Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

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	AGGTTAATAA	CGAGCTATGT	AGGCAAAGCT	GGGTTGAGTA	ATATCGTAAG
3851	GCAGCACTCT CGTCGTGAGA	TCGCATGGAG AGCGTACCTC	TTGATGGGCT AACTACCCGA	GTGATTTAAA CACTAAATTT	TAGTTGCAGC ATCAACGTCG
3901	ATGCCATTGG	GAATGGAGAG	TAAAGCAATA	TCAGATGCAC	AGATTACTGC
3301	TACGGTAACC	CTTACCTCTC	ATTTCGTTAT	AGTCTACGTG	TCTAATGACG
3951	TTCATCCTAC	TTTACCAATA	TGTTTGCCAC	CTGGTCTCCT	TCAAAAGCTC
4001	AAGTAGGATG	AAATGGTTAT	ACAAACGGTG	GACCAGAGGA	AGTTTTCGAG
4001	GACTTCACCT CTGAAGTGGA	CCAAGGGAGG GGTTCCCTCC	AGTAATGCCT TCATTACGGA	GGAGACCTCA CCTCTGGAGT	GGTGAATAAT CCACTTATTA
4051	CCAAAAGAGT	GGCTGCAAGT	GGACTTCCAG	AAGACAATGA	AAGTCACAGG
100-	GGTTTTCTCA	CCGACGTTCA	CCTGAAGGTC	TTCTGTTACT	TTCAGTGTCC
4101	AGTAACTACT	CAGGGAGTAA	AATCTCTGCT	TACCAGCATG	TATGTGAAGG
<b>4151</b>	TCATTGATGA AGTTCCTCAT	GTCCCTCATT CTCCAGCAGT	TTAGAGACGA CAAGATGGCC	ATGGTCGTAC ATCAGTGGAC	ATACACTTCC TCTCTTTTTT
4151	TCAAGGAGTA	GAGGTCGTCA	GTTCTACCGG	TAGTCACCTG	AGAGAAAAA
4201	CAGAATGGCA	AAGTAAAGGT	TTTTCAGGGA	AATCAAGACT	CCTTCACACC
	GTCTTACCGT	TTCATTTCCA	AAAACTCCCT	TTAGTTCTGA	GGAAGTGTGG
4251	TGTGGTGAAC	TCTCTAGACC	CACCGTTACT	GACTCGCTAC	CTTCGAATTC
4301	ACACCACTTG ACCCCCAGAG	AGAGATCTGG TTGGGTGCAC	GTGGCAATGA CAGATTGCCC	CTGAGCGATG TGAGGATGGA	GAAGCTTAAG GGTTCTGGGC
420T	TGGGGGTCTC	AACCCACGTG	GTCTAACGGG	ACTCCTACCT	CCAAGACCCG
4351	TGCGAGGCAC	AGGACCTCTA	C		331213110000
	ACGCTCCGTG	TCCTGGAGAT	G		

1-57 SIGNAL PEPTIDE 58-1173 A1 DOMAIN 1174-2277 A2 DOMAIN 2278-2319 SQ LINKER 2320-3432 ap-A3 DOMAINS 3433-3891 C1 DOMAIN 3892-4371 C2 DOMAIN

FIG. 7D

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#### AMINO ACID SEQUENCE OF HP47/OL

```
LSWDYRQSEL LRELHVDTRF
      MOLELSTCVF
                  LCLLPLGFSA
                              IRRYYLGAVE
 51
                                          VARPRPPWMG
      PATAPGALPL
                  GPSVLYKKTV
                              FVEFTDOLFS
                                                      LLGPTIOAEV
 101
      YDTVVVTLKN
                  MASHPVSLHA
                              VGVSFWKSSE
                                          GAEYEDHTSQ
                                                      REKEDDKVLP
                                          HVDLVKDLNŠ
 151
      GKSOTYVWOV
                  LKENGPTASD
                              PPCLTYSYLS
                                                      GLIGALLVCR
\bar{2}01
      EGSLTRERTO
                  NLHEFVLLFA
                              VFDEGKSWHS
                                          ARNDSWTRAM
                                                      DPAPARAQPA
 251
      MHTVNGYVNR
                  SLPGLIGCHK
                              KSVYWHVIGM
                                          GTSPEVHSIF
                                                      LEGHTFLVRH
301
                              MDLGQFLLFC
      HRQASLEISP
                  LTFLTAQTFL
                                          HISSHHHGGM
                                                      EAHVRVESCA
 351
      EEPQLRRKAD
                  EEEDYDDNLY
                              DSDMDVVRLD
                                          GDDVSPFIQI
                                                      RSVAKKHPKT
 401
                  DWDYAPLVLA
                              PDDRSYKSQY
                                          LNNGPQRIĞR
                                                      KYKKVRFMAY
      WVHYIAAEEE
 451
                              LLYGEVGDTL
                                                      PYNIYPHGIT
                  IQHESGILGP
                                          LIIFKNOASR
      TDETFKTREA
 501
                              PILPGEIFKY
                                          KWTVTVEDGP
                                                      TKSDPRCLTR
      DVRPLYSRRL
                  PKGVKHLKDF
 551
                                          RGNOIMSDKR
                                                      NVILFSVFDE
      YYSSFVNMER
                  DLASGLIGPL
                              LICYKESVDO
 601
                              QLEDPEFQAS
      NRSWYLTENI
                  ORFLPNPAGV
                                          NIMHSINGYV
                                                      FDSLQLSVCL
 651
                                                      PFSGETVFMS
      HEVAYWYILS
                  IGAOTDFLSV
                              FFSGYTFKHK
                                          MVYEDTLTLF
                                          DKNTGDYYED
 701
                  CHNŜDFRNRG
      MENPGLWILG
                              MTALLKVSSC
                                                      SYEDISAYLL
 751
                              SAPKPPVLRR
                                          HORDISLPTF
                                                      QPEEDKMDYD
      SKNNAIEPRS
                  FAONSRPPSA
 801
      DIFSTETKGE
                  DFDIYGEDEN
                              QDPRSFQKRT
                                          RHYFIAAVEQ
                                                      LWDYGMSESP
 851
                              REFADGSFTO
      RALRNRAQNG
                  EVPRFKKVVF
                                          PSYRGELNKH
                                                      LGLLGPYIRA
 901
                                          QEQGAEPRHN
                                                      FVQPNETRTY
      EVEDNIMVTF
                  KNQASRPYSF
                              YSSLISYPDD
 951
      FWKVQHHMAP
                  TEÕEFDCKAW
                                          DVHSGLIGPL
                                                      LIĈRANTLNA
                              AYFSDVDLEK
                              TKSWYFTENV
1001
      AHGROVTVQE
                  FALFFTIFDE
                                          ERNCRAPCHL
                                                      QMEDPTLKEN
                                                      ĨHFSGHVFSV
      YRFHÄINGŸV
                                          SMGSNENIHS
1051
                  MDTLPGLVMA
                              ONORIRWYLL
                              VEMLPSKVGI
                                          WRIECLIGEH
                                                      LOAGMSTTFL
1101
      RKKEEYKMAV
                  YNLYPGVFET
1151
      VYSKKCQTPL
                              QITASGQYGQ
                                          WAPKLARLHY
                                                      SGSINAWSTK
                  GMASGHIRDF
1201
1251
                              TOGAROKFSŠ
      EPFSWIKVDL
                  LAPMIIHGIK
                                          LYISOFIIMY
                                                      SLDGKKWQTY
                                          ARYIÑLHPTH
                                                      YSIRSTLRME
      RGNSTGTLMV
                  FFGNVDSSGI
                              KHNIFNPPII
                              SDAQITASSY
1301
      LMGCDLNSCS
                  MPLGMESKAI
                                          FTNMFATWSP
                                                      SKARLHLQGR
1351
                  PKEWLQVDFO
                              KTMKVTGVTT
                                          OGVKSLLTSM
                                                      YVKEFLISSS
      SNAWRPQVNN
1401
      QDGHQWTLFF
                  QNGKVKVFQG
                              NODSFTPVVN
                                          SLDPPLLTRY LRIHPQSWVH
1451
      OIALRMEVLG
                  CEAQDLY*
```

1-19 SIGNAL PEPTIDE 20-391 A1 DOMAIN 392-759 A2 DOMAIN 760-783 OL LINKER 784-1154 ap-A3 1155-1307 C1 DOMAIN 1308-1467 C2 DOMAIN

Inventor(s): Lollar
Application No: To be Assigned
Atty Dkt No: 007157/276516

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## HP47/OL NUCLEOTIDE SEQUENCE

1	ATGCAGCTAG	AGCTCTCCAC	CTGTGTCTTT	CTGTGTCTCT	TGCCACTCGG
_	TACGTCGATC	TCGAGAGGTG		GACACAGAGA	
51	CTTTAGTGCC	ATCAGGAGAT	ACTACCTGGG	CGCAGTGGAA	CTGTCCTGGG
	GAAATCACGG	TAGTCCTCTA	TGATGGACCC	GCGTCACCTT	GACAGGACCC
101	ACTACCGGCA	AAGTGAACTC	CTCCGTGAGC	TGCACGTGGA	CACCAGATTT
	TGATGGCCGT	TTCACTTGAG	GAGGCACTCG	ACGTGCACCT	GTGGTCTAAA
151	CCTGCTACAG	CGCCAGGAGC	TCTTCCGTTG	GGCCCGTCAG	TCCTGTACAA
	GGACGATGTC	GCGGTCCTCG	AGAAGGCAAC	CCGGGCAGTC	AGGACATGTT
201	AAAGACTGTG	TTCGTAGAGT	TCACGGATCA	ACTTTTCAGC	GTTGCCAGGC
	TTTCTGACAC	AAGCATCTCA	AGTGCCTAGT	TGAAAAGTCG	CAACGGTCCG
251	CCAGGCCACC	ATGGATGGGT	CTGCTGGGTC	CTACCATCCA	GGCTGAGGTT
	GGTCCGGTGG	TACCTACCCA	GACGACCCAG	GATGGTAGGT	CCGACTCCAA
301	TACGACACGG	TGGTCGTTAC	CCTGAAGAAC	ATGGCTTCTC	ATCCCGTTAG
	ATGCTGTGCC	ACCAGCAATG	GGACTTCTTG	TACCGAAGAG	TAGGGCAATC
351	TCTTCACGCT	GTCGGCGTCT	CCTTCTGGAA	ATCTTCCGAA	GGCGCTGAAT
	AGAAGTGCGA	CAGCCGCAGA	GGAAGACCTT	TAGAAGGCTT	CCGCGACTTA
401	ATGAGGATCA	CACCAGCCAA	AGGGAGAAGG	AAGACGATAA	AGTCCTTCCC
	TACTCCTAGT	GTGGTCGGTT	TCCCTCTTCC	TTCTGCTATT	TCAGGAAGGG
451	GGTAAAAGCC	AAACCTACGT	CTGGCAGGTC	CTGAAAGAAA	ATGGTCCAAC
	CCATTTTCGG	TTTGGATGCA	GACCGTCCAG	GACTTTCTTT	TACCAGGTTG
501	AGCCTCTGAC	CCACCATGTC	TTACCTACTC	ATACCTGTCT	CACGTGGACC
	TCGGAGACTG	GGTGGTACAG	AATGGATGAG	TATGGACAGA	GTGCACCTGG
551	TGGTGAAAGA	CCTGAATTCG	GGCCTCATTG	GAGCCCTGCT	GGTTTGTAGA
	ACCACTTTCT	GGACTTAAGC	CCGGAGTAAC	CTCGGGACGA	CCAAACATCT
601	GAAGGGAGTC	TGACCAGAGA	AAGGACCCAG	AACCTGCACG	AATTTGTACT
	CTTCCCTCAG	ACTGGTCTCT	TTCCTGGGTC	TTGGACGTGC	TTAAACATGA
651	ACTTTTTGCT	GTCTTTGATG	AAGGGAAAAG	TTGGCACTCA	GCAAGAAATG
	TGAAAAACGA	CAGAAACTAC	TTCCCTTTTC	AACCGTGAGT	CGTTCTTTAC
701	ACTCCTGGAC	ACGGGCCATG	GATCCCGCAC	CTGCCAGGGC	CCAGCCTGCA
	TGAGGACCTG	TGCCCGGTAC	CTAGGGCGTG	GACGGTCCCG	GGTCGGACGT
751	ATGCACACAG	TCAATGGCTA	TGTCAACAGG	TCTCTGCCAG	GTCTGATCGG
	TACGTGTGTC	AGTTACCGAT	ACAGTTGTCC	AGAGACGGTC	CAGACTAGCC
801	ATGTCATAAG	AAATCAGTCT	ACTGGCACGT	GATTGGAATG	GGCACCAGCC
0.51	TACAGTATTC	TTTAGTCAGA	TGACCGTGCA	CTAACCTTAC	CCGTGGTCGG
851	CGGAAGTGCA	CTCCATTTTT	CTTGAAGGCC	ACACGTTTCT	CGTGAGGCAC
001	GCCTTCACGT	GAGGTAAAAA	GAACTTCCGG	TGTGCAAAGA	GCACTCCGTG
901	CATCGCCAGG	CTTCCTTGGA	GATCTCGCCA	CTAACTTTCC	TCACTGCTCA
0.51	GTAGCGGTCC	GAAGGAACCT	CTAGAGCGGT	GATTGAAAGG	AGTGACGAGT
951	GACATTCCTG	ATGGACCTTG	GCCAGTTCCT	ACTGTTTTGT	CATAICICII
1001		TACCTGGAAC		TGACAAAACA	
1001	CCCACCACCA		GAGGCTCACG		AAGCTGCGCC
1051		ACCACCGTAC	CTCCGAGTGC	AGTCTCATCT	
1051		AGCTGCGGAG	GAAAGCTGAT	GAAGAGGAAG	ATTATGATGA TAATACTACT
1101		TCGACGCCTC	CTTTCGACTA	CTTCTCCTTC	
1101	CAATTTGTAC GTTAAACATG		TGGACGTGGT	CCGGCTCGAT GGCCGAGCTA	GGTGACGACG CCACTGCTGC
1151		CTGAGCCTGT TATCCAAATC	ACCTGCACCA CGCTCGGTTG	CCAAGAAGCA	TCCTAAAACT
1151		ATAGGTTTAG	GCGAGCCAAC	GGTTCTTCGT	AGGATTTTGA
1201		ACATTGCTGC	TGAAGAGGAG		ATGCTCCCTT
1201	IGGGIACHII	WCHI I GC I GC	DADDADAADI	IJAUUUIJAU	VIQCICCCII

		mama a aaa aa	* CDDCCCCC	CENCIA COCENCIA	ma
	ACCCATGTAA		ACTTCTCCTC	CTGACCCTGA	TACGAGGGAA
1251	AGTCCTCGCC	CCCGATGACA	GAAGTTATAA	AAGTCAATAT	TTGAACAATG
	TCAGGAGCGG	GGGCTACTGT	CTTCAATATT	TTCAGTTATA	AACTTGTTAC
1301	GCCCTCAGCG	GATTGGTAGG	AAGTACAAAA	AAGTCCGATT	TATGGCATAC
1001	CGGGAGTCGC		TTCATGTTTT	TTCAGGCTAA	ATACCGTATG
- 2		CTAACCATCC			
1351	ACAGATGAAA	CCTTTAAGAC	GCGTGAAGCT	ATTCAGCATG	AATCAGGAAT
	TGTCTACTTT	GGAAATTCTG	CGCACTTCGA	TAAGTCGTAC	TTAGTCCTTA
1401	CTTGGGACCT	TTACTTTATG	GGGAAGTTGG	AGACACACTG	TTGATTATAT
1101	GAACCCTGGA	AATGAAATAC	CCCTTCAACC	TCTGTGTGAC	AACTAATATA
1 1 5 1					CGGAATCACT
1451	TTAAGAATCA	AGCAAGCAGA	CCATATAACA	TCTACCCTCA	
	AATTCTTAGT	TCGTTCGTCT	GGTATATTGT	AGATGGGAGT	GCCTTAGTGA
1501	GATGTCCGTC	CTTTGTATTC	AAGGAGATTA	CCAAAAGGTG	TAAAACATTT
	CTACAGGCAG	GAAACATAAG	TTCCTCTAAT	GGTTTTCCAC	ATTTTGTAAA
1001			CAGGAGAAAT	ATTCAAATAT	AAATGGACAG
1551	GAAGGATTTT	CCAATTCTGC			
	CTTCCTAAAA	GGTTAAGACG	GTCCTCTTTA	TAAGTTTATA	TTTACCTGTC
1601	TGACTGTAGA	AGATGGGCCA	ACTAAATCAG	ATCCGCGGTG	CCTGACCCGC
	ACTGACATCT	TCTACCCGGT	TGATTTAGTC	TAGGCGCCAC	GGACTGGGCG
1651	TATTACTCTA	GTTTCGTTAA	TATGGAGAGA	GATCTAGCTT	CAGGACTCAT
1001			ATACCTCTCT	CTAGATCGAA	GTCCTGAGTA
	ATAATGAGAT	CAAAGCAATT			
1701	TGGCCCTCTC	CTCATCTGCT	ACAAAGAATC	TGTAGATCAA	AGAGGAAACC
	ACCGGGAGAG	GAGTAGACGA	TGTTTCTTAG	ACATCTAGTT	TCTCCTTTGG
1751	AGATAATGTC	AGACAAGAGG	AATGTCATCC	TGTTTTCTGT	ATTTGATGAG
1,01	TCTATTACAG	TCTGTTCTCC	TTACAGTAGG	ACAAAAGACA	TAAACTACTC
1001					
1801	AACCGAAGCT	GGTACCTCAC	AGAGAATATA	CAACGCTTTC	TCCCCAATCC
	TTGGCTTCGA	CCATGGAGTG	TCTCTTATAT	GTTGCGAAAG	AGGGGTTAGG
1851	AGCTGGAGTG	CAGCTTGAGG	ATCCAGAGTT	CCAAGCCTCC	AACATCATGC
	TCGACCTCAC	GTCGAACTCC	TAGGTCTCAA	GGTTCGGAGG	TTGTAGTACG
1901	ACAGCATCAA	TGGCTATGTT	TTTGATAGTT	TGCAGTTGTC	AGTTTGTTTG
1701	TGTCGTAGTT	ACCGATACAA	AAACTATCAA	ACGTCAACAG	TCAAACAAAC
1951	CATGAGGTGG	CATACTGGTA	CATTCTAAGC	ATTGGAGCAC	AGACTGACTT
	GTACTCCACC	GTATGACCAT	GTAAGATTCG	TAACCTCGTG	TCTGACTGAA
2001	CCTTTCTGTC	TTCTTCTCTG	GATATACCTT	CAAACACAAA	ATGGTCTATG
	GGAAAGACAG	AAGAAGAGAC	CTATATGGAA	GTTTGTGTTT	TACCAGATAC
2051	AAGACACACT	CACCCTATTC	CCATTCTCAG	GAGAAACTGT	CTTCATGTCG
2031					GAAGTACAGC
	TTCTGTGTGA	GTGGGATAAG	GGTAAGAGTC	CTCTTTGACA	
2101	ATGGAAAACC	CAGGTCTATG	GATTCTGGGG	TGCCACAACT	CAGACTTTCG
	TACCTTTTGG	GTCCAGATAC	CTAAGACCCC	ACGGTGTTGA	GTCTGAAAGC
2151	GAACAGAGGC	ATGACCGCCT	TACTGAAGGT	TTCTAGTTGT	GACAAGAACA
	CTTGTCTCCG	TACTGGCGGA		AAGATCAACA	
2201	CTGGTGATTA	TTACGAGGAC	AGTTATGAAG	ATATTTCAGC	ATACTTGCTG
2201					
	GACCACTAAT	TTACGAGGAC	TCAATACTTC	TATAAAGTCG	TATGAACGAC
2251	AGTAAAAACA	ATGCCATTGA	ACCTAGGAGC	TTTGCCCAGA	ATTCAAGACC
	TCATTTTTGT	TACGGTAACT	TGGATCCTCG	AAACGGGTCT	TAAGTTCTGG
2301		AGCGCTCCAA		CCTGCGACGG	CATCAGAGGG
2301	GGGATCACGC	TCGCGAGGTT	TCGGAGGCCA	GGACGCTGCC	GTAGTCTCCC
0251					
2351	ACATAAGCCT	TCCTACTTTT	CAGCCGGAGG	AAGACAAAAT	GGACTATGAT
	TGTATTCGGA	AGGATGAAAA	GTCGGCCTCC	TTCTGTTTTA	
2401	GATATCTTCT	CAACTGAAAC	GAAGGGAGAA	GATTTTGACA	TTTACGGTGA
		GTTGACTTTG	CTTCCCTCTT	CTAAAACTGT	AAATGCCACT
2/51	GGATGAAAAT	CAGGACCCTC	GCAGCTTTCA	GAAGAGAACC	CGACACTATT
2451					
0.5.0	CCTACTTTTA		CGTCGAAAGT	CTTCTCTTGG	GCTGTGATAA
2501	TCATTGCTGC	GGTGGAGCAG	CTCTGGGATT	ACGGGATGAG	CGAATCCCCC

Inventor(s): Lollar Application No: To be Assigned Atty Dkt No: 007157/276516

2551	AGTAACGACG CGGGCGCTAA	CCACCTCGTC GAAACAGGGC	GAGACCCTAA TCAGAACGGA AGTCTTGCCT	TGCCCTACTC GAGGTGCCTC CTCCACGGAG	GCTTAGGGGG GGTTCAAGAA CCAAGTTCTT
2601	GCCCGCGATT GGTGGTCTTC CCACCAGAAG	CTTTGTCCCG CGGGAATTTG GCCCTTAAAC	CTGACGGCTC GACTGCCGAG	CTCCACGGAG CTTCACGCAG GAAGTGCGTC	CCAAGTTCTT CCGTCGTACC GGCAGCATGG
2651	GCGGGGAACT	CAACAAACAC	TTGGGGCTCT	TGGGACCCTA	CATCAGAGCG
	CGCCCCTTGA	GTTGTTTGTG	AACCCCGAGA	ACCCTGGGAT	GTAGTCTCGC
2701	GAAGTTGAAG	ACAACATCAT	GGTAACTTTC	AAAAACCAGG	CGTCTCGTCC
	CTTCAACTTC	TGTTGTAGTA	CCATTGAAAG	TTTTTTGGTCC	GCAGAGCAGG
2751	CTATTCCTTC	TACTCGAGCC	TTATTTCTTA	TCCGGATGAT	CAGGAGCAAG
	GATAAGGAAG	ATGAGCTCGG	AATAAAGAAT	AGGCCTACTA	GTCCTCGTTC
2801	GGGCAGAACC	TCGACACAAC	TTCGTCCAGC	CAAATGAAAC	CAGAACTTAC
	CCCGTCTTGG	AGCTGTGTTG	AAGCAGGTCG	GTTTACTTTG	GTCTTGAATG
2851	TTTTGGAAAG	TGCAGCATCA	CATGGCACCC	ACAGAAGACG	AGTTTGACTG
	AAAACCTTTC	ACGTCGTAGT	GTACCGTGGG	TGTCTTCTGC	TCAAACTGAC
2901	CAAAGCCTGG	GCCTACTTTT	CTGATGTTGA	CCTGGAAAAA	GATGTGCACT
	GTTTCGGACC	CGGATGAAAA	GACTACAACT	GGACCTTTTT	CTACACGTGA
2951	CAGGCTTGAT	CGGCCCCCTT	CTGATCTGCC	GCGCCAACAC	CCTGAACGCT
	GTCCGAACTA	GCCGGGGGAA	GACTAGACGG	CGCGGTTGTG	GGACTTGCGA
3001	GCTCACGGTA	GACAAGTGAC	CGTGCAAGAA	TTTGCTCTGT	TTTTCACTAT
	CGAGTGCCAT	CTGTTCACTG	GCACGTTCTT	AAACGAGACA	AAAAGTGATA
3051	TTTTGATGAG	ACAAAGAGCT	GGTACTTCAC	TGAAAATGTG	GAAAGGAACT
	AAAACTACTC	TGTTTCTCGA	CCATGAAGTG	ACTTTTACAC	CTTTCCTTGA
3101	GCCGGGCCCC	CTGCCATCTG	CAGATGGAGG	ACCCCACTCT	GAAAGAAAAC
	CGGCCCGGGG	GACGGTAGAC	GTCTACCTCC	TGGGGTGAGA	CTTTCTTTTG
3151	TATCGCTTCC	ATGCAATCAA	TGGCTATGTG	ATGGATACAC	TCCCTGGCTT
	ATAGCGAAGG	TACGTTAGTT	ACCGATACAC	TACCTATGTG	AGGGACCGAA
3201	AGTAATGGCT	CAGAATCAAA	GGATCCGATG	GTATCTGCTC	AGCATGGGCA
	TCATTACCGA	GTCTTAGTTT	CCTAGGCTAC	CATAGACGAG	TCGTACCCGT
3251	GCAATGAAAA	TATCCATTCG	ATTCATTTTA	GCGGACACGT	GTTCAGTGTA
	CGTTACTTTT	ATAGGTAAGC	TAAGTAAAAT	CGCCTGTGCA	CAAGTCACAT
3301	CGGAAAAAGG	AGGAGTATAA	AATGGCCGTG	TACAATCTCT	ATCCGGGTGT
	GCCTTTTTCC	TCCTCATATT	TTACCGGCAC	ATGTTAGAGA	TAGGCCCACA
3351	CTTTGAGACA	GTGGAAATGC	TACCGTCCAA	AGTTGGAATT	TGGCGAATAG
	GAAACTCTGT	CACCTTTACG	ATGGCAGGTT	TCAACCTTAA	ACCGCTTATC
3401	AATGCCTGAT	TGGCGAGCAC	CTGCAAGCTG	GGATGAGCAC	GACTTTCCTG
	TTACGGACTA	ACCGCTCGTG	GACGTTCGAC	CCTACTCGTG	CTGAAAGGAC
3451		AGAAGTGTCA TCTTCACAGT	GACTCCCCTG CTGAGGGGAC		
3501		GTCTAATGTC	CTTCAGGACA GAAGTCCTGT		TGGGCCCCAA ACCCGGGGTT
3551	TCGACCGGTC		TCCGGATCAA AGGCCTAGTT	AGTTACGGAC	GAGCACCAAG CTCGTGGTTC
3601		GAACCTAGTT	GGTGGATCTG CCACCTAGAC		TGATTATTCA ACTAATAAGT
3651	GCCGTAGTTC	ACCCAGGGTG TGGGTCCCAC	CCCGTCAGAA GGGCAGTCTT	CAAGAGGTCG	GAGATGTAGA
3701	GAGTCAAATA		AGTCTTGATG TCAGAACTAC	GGAAGAAGTG CCTTCTTCAC	CGTCTGAATA
3751	CGAGGAAATT GCTCCTTTAA	CCACTGGAAC GGTGACCTTG	CTTAATGGTC GAATTACCAG	TTCTTTGGCA AAGAAACCGT	TACACCTAAG
3801	ATCTGGGATA	AAACACAATA	TTTTTAACCC	TCCAATTATT	GCTCGATACA

	TAGACCCTAT	TTTGTGTTAT	AAAAATTGGG	AGGTTAATAA	CGAGCTATGT
3851	TCCGTTTGCA	CCCAACTCAT	TATAGCATTC	GCAGCACTCT	TCGCATGGAG
3901	AGGCAAACGT TTGATGGGCT	GGGTTGAGTA GTGATTTAAA	ATATCGTAAG TAGTTGCAGC	CGTCGTGAGA ATGCCATTGG	AGCGTACCTC GAATGGAGAG
J J U I	AACTACCCGA	CACTAAATTT	ATCAACGTCG	TACGGTAACC	CTTACCTCTC
3951	TAAAGCAATA	TCAGATGCAC	AGATTACTGC	TTCATCCTAC	TTTACCAATA
	ATTTCGTTAT	AGTCTACGTG	TCTAATGACG	AAGTAGGATG	AAATGGTTAT
4001	TGTTTGCCAC	CTGGTCTCCT	TCAAAAGCTC	GACTTCACCT	CCAAGGGAGG
4051	ACAAACGGTG	GACCAGAGGA	AGTTTTCGAG	CTGAAGTGGA	GGTTCCCTCC
4051	AGTAATGCCT TCATTACGGA	GGAGACCTCA	GGTGAATAAT CCACTTATTA	CCAAAAGAGT	GGCTGCAAGT
4101	GGACTTCCAG	CCTCTGGAGT AAGACAATGA	AAGTCACAGG	GGTTTTCTCA AGTAACTACT	CCGACGTTCA CAGGGAGTAA
4101	CCTGAAGGTC	TTCTGTTACT	TTCAGTGTCC	TCATTGATGA	GTCCCTCATT
4151	AATCTCTGCT	TACCAGCATG	TATGTGAAGG	AGTTCCTCAT	CTCCAGCAGT
1101	TTAGAGACGA	ATGGTCGTAC	ATACACTTCC	TCAAGGAGTA	GAGGTCGTCA
4201	CAAGATGGCC	ATCAGTGGAC	TCTCTTTTTT	CAGAATGGCA	AAGTAAAGGT
	GTTCTACCGG	TAGTCACCTG	AGAGAAAAA	GTCTTACCGT	TTCATTTCCA
4251	TTTTCAGGGA	AATCAAGACT	CCTTCACACC	TGTGGTGAAC	TCTCTAGACC
4201	AAAAGTCCCT	TTAGTTCTGA	GGAAGTGTGG	ACACCACTTG	AGAGATCTGG
4301	CACCGTTACT	GACTCGCTAC	CTTCGAATTC	ACCCCCAGAG	TTGGGTGCAC
4351	GTGGCAATGA CAGATTGCCC	CTGAGCGATG TGAGGATGGA	GAAGCTTAAG GGTTCTGGGC	TGGGGGTCTC TGCGAGGCAC	AACCCACGTG AGGACCTCTA
4331	GTCTAACGGG	ACTCCTACCT	CCAAGACCCG	ACGCTCCGTG	TCCTGGAGAT
4401	C	ACICCIACCI	DJJJADALJJ	ACGCICCGIG	ICCIGGAGAI
1101	Ğ				
	-				

FIG. 9D

Inventor(s): Lollar Application No: To be Assigned Atty Dkt No: 007157/276516

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AMINO ACID SEQUENCE OF HUMAN B DOMAIN-DELETED FACTOR VIII (HSQ) Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Tyr Tyr Leu Gly Ala Val Glu Leu Ser Cys Phe Ser Ala Thr Arg Arg 'yr Met Gin Ser Asp Leu Gly Giu Leu Pro Val Asp Ala Arg Lys Ser Phe Pro Phe Asn Thr Ser Val Phe Pro Pro Arg Val Pro Val His Leu Phe Phe Val Glu Phe Thr Lys Lys ьeu Gly Leu Leu Gly Arg Pro Pro Trp Met GIn Ile Thr Leu Lys Ala Ser Tyr Asp Asn Met Ala Glu Val Tyr Val Val 105 110 Ser Leu His Ala Val Gly Val Ser Lys Ala His Pro Val 120 Glu Gly Ala Glu Thr Asp Asp Gln Thr Ser 130 Gln Arg Glu Lys Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu 155 160 Pro Met Ala Ser Asp Pro Leu Cys Leu Ser Gly 170 Lys Asp Leu Asn Ser 185 Val Asp Leu Val Gly Leu Ile Tyr Leu Ser His 190 180 Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys 205 195 200 Phe Ile Leu Leu Phe Ala Val Phe Asp Glu GIn Thr Leu His Lys 215 220 210 Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Thr Val Asn Giy Arg Ala Trp Pro Lys Met His Ala 250 Ser Leu Pro Gly Leu Ile Gly Cys Ser Asn Arg 260 265 Gly Thr Thr Pro Glu Val His Ser Trp His Val Ile Gly Met 280 285 275 Phe Leu Val Arg Phe Leu Glu Gly His Asn His Arg Gln Ala Thr 295 290 300 Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Leu Glu Ile Ser 310 315 320 305 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His 330 35 325 Lys Val Asp Ser Cys Pro Glu Glu Pro Gly Met Glu Ala Tyr Val 345 Asn Asn Glu Glu Ala Glu Asp Gln Leu Arg Met Lys Asp Asp 360 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp 370 380 Asp Asp Asn Gln Ile Arg Ser Val Ala Lys Thr Pro Ser Lys Hıs 395 390 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro

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Τ	1127	Lou	אן א	405	λας	7 00			410	Two	Cor	Cln	ጥኒኒዮ	415	λan
	Val		420					425					430		
Asn	Gly	Pro 435	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val 445	Arg	Phe	Met
Ala	Tyr 450		Asp	Glu	Thr	Phe 455	Lys	Thr	Arg	Glu	Ala 460	Īle	Gln	His	Glu
Ser	Gly	Ile	Leu	Gly	Pro 470		Leu	Tyr	Gly	Glu 475		Gly	Asp	Thr	Leu 480
465 Leu	Ile	Ile	Phe	Lys 485		Gln	Ala	Ser	Arg 490		Tyr	Asn	Ile	Tyr	Pro
His	Gly	Ile			Val	Arg	Pro	Leu		Ser	Arg	Arg		Pro	Lys
Gly	Val	Lys	500 His	Leu	Lys	Asp	Phe	505 Pro	Ile	Leu	Pro	Gly	510 Glu	Ile	Phe
Lys	Tyr	Lys	Trp	Thr	Val	Thr 535	520 Val	Glu	Asp	Gly	Pro 540	525 Thr	Lys	Ser	Asp
Pro	Arg	Cys	Leu	Thr	Arg		Tyr	Ser	Ser	Phe 555		Asn	Met	Glu	Arg 560
545 Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu 570		Ile	Cys	Tyr	Lys 575	
Ser	Val	Asp		Arg	Gly	Asn	Gln	Ile		Ser	Asp	Lys	Arg 590		Val
Ile	Leu	Phe	580 Ser	Val	Phe	Asp	Glu	585 Asn	Arg	Ser	Trp	Tyr		Thr	Glu
Asn	Ile 610	595 Gln	Arg	Phe	Leu	Pro 615	600 Asn	Pro	Ala	Gly	Val 620	605 Gln	Leu	Glu	Asp
	Glu	Phe	Gln	Ala			Ile	Met	His	Ser 635		Asn	Gly	Tyr	Val 640
625 Phe	Asp	Ser	Leu	Gln 645	630 Leu	Ser	Val	Cys	Leu 650		Glu	Val	Ala	Tyr	Trp
Tyr	· Ile	Leu	Ser 660		Gly	Ala	Gln	Thr 665		Phe	Leu	Ser	Val 670	Phe	Phe
Ser	Gly	Tyr		Phe	Lys	His			Val	Tyr	Glu	Asp		Leu	Thr
Let	Phe 690	Pro	Phe	Ser	Gly	Glu 695	680 Thr	Val	Phe	Met	Ser 700		Glu	Asn	Pro
Gly 705	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly 720
Met	7														
Tyr	Tyr	Glu	Asp 740		Tyr	Glu	Asp	Ile 745		Ala	Tyr	Leu	Leu 750	Ser	Lys
Asr	Asn	Ala 755		Glu	Pro	Arg			Ser	Gln	Asn	Pro 765		Val	Leu
Lys	Arg		Gln	Arg	Glu	Ile 775	760 Thr	Arg	Thr	Thr	Leu 780	Gln	Ser	Asp	Gln
Gli 785	Glu	Ile	Asp	Tyr	Asp		Thr	Ile	Ser	Val 795		Met	Lys	Lys	Glu 800
	Phe	Asp	Ile	Tyr 805	Asp	Glu	Asp	Glu	Asn 810		Ser	Pro	Arg	Ser 815	Phe
Glr	Lys	Lys	Thr 820		His	Hyr	Phe	Ile 825		Ala	Val	Glu	Arg 830		Trp
Asp	Tyr	Gly 835		Ser	Ser	Ser	Pro 840		Val	Leu	Arg	Asn 845		Ala	Gln
Sei	Gly 850		Val	Pro	Gln	Phe 855	Lys		Val	Val	Phe 860		Glu	Phe	Thr
							7 - 1	$I \cap D$							

FIG. 10B

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26/33 Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His 870 Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn 895 Val Thr Phe Arq Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser 905 900 910 Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg 920 915 925 Pro Asn Glu Thr Lys Tyr Phe Trp Lys Lys Asn Phe Val Lys Thr 940 930 935 Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Gln His His 960 950 955 Ser Asp Val Asp Leu Glu Lys Asp Val His Gly Leu 975 965 970 Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His 990 980 985 Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Arg Gln Val Thr 995 1000 1005 Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Asp Glu Thr Lys Ser Trp 1015 1020 1010 Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn 1035 1040 1025 1030 Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro\_Gly 1045 1050 Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met 1065 1070 1060 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe 1085 1080 1075 Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr 1090 1095 1100 Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly 1115 1120 1110 1105 Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser 1125 1130 1135 Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met 1145 1140 1150 Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr 1155 1165 1160 Tyr Ser Gly Ser lie Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His 1180 1175 Trp Ile Lys Val Asp Leu Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser 1195 1190 1200 1185 Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln 1205 1210 1215 Leu Ala Pro Met Tyr Ser Leu 1230 Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met 1220 1225 Tyr Arg Gly Ash Ser Thr Gly Thr Leu 1240 1245 Lys Lys 1235 Trp Gln Thr Ile Lys His Asn He Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly 1255 1260 1250 Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His 1265 1270 1275 1280 Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu 1285 1295 1290 Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp 1300 1310 1305 Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp

FIG. 10C

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1315 1320 1325 Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp 1330 1335 1340 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln 1355 1350 Thr Thr Gln Gly Val Lys Val Thr Gly Val Ser Leu 1365 1375 1370 Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser 1380 Ser Gln Asp 1390 Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe 1395 1400 1405 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro 1410 1415 1420 Tyr Leu Arg Ile His Pro Gln Ser Trp Val His 1430 1435 1440 Pro Leu Leu Thr Arq Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu
1445 1450 1455 Tyr

FIG. 10D

Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

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# NUCLEOTIDE SEQUENCE OF HUMAN B DOMAIN-DELETED FACTOR VIII (HSQ)

_		- aamamaa.a	ama ammamm	amama aammm	ma aa x mm ama
1	· · · · · - <del>-</del> - · · · · - · ·	AGCTCTCCAC		CTGTGCCTTT	
51	CTTTAGTGCC	ACCAGAAGAT	ACTACCTGGG	TGCAGTGGAA	CTGTCATGGG
101	ACTATATGCA	AAGTGATCTC	GGTGAGCTGC	CTGTGGACGC	AAGATTTCCT
151	CCTAGAGTGC	CAAAATCTTT	TCCATTCAAC	ACCTCAGTCG	TGTACAAAAA
201	GACTCTGTTT	GTAGAATTCA	CGGTTCACCT	TTTCAACATC	GCTAAGCCAA
				CCATCCAGGC	TGAGGTTTAT
251	GGCCACCCTG	GATGGGTCTG	CTAGGTCCTA		
301	GATACAGTGG	TCATTACACT	TAAGAACATG	GCTTCCCATC	CTGTCAGTCT
351	TCATGCTGTT	GGTGTATCCT	ACTGGAAAGC	TTCTGAGGGA	GCTGAATATG
401	ATGATCAGAC	CAGTCAAAGG	GAGAAAGAAG	ATGATAAAGT	CTTCCCTGGT
451	GGAAGCCATA	CATATGTCTG	GCAGGTCCTG	AAAGAGAATG	GTCCAATGGC
501	CTCTGACCCA	CTGTGCCTTA	CCTACTCATA	TCTTTCTCAT	GTGGACCTGG
551	TAAAAGACTT	GAATTCAGGC	CTCATTGGAG	CCCTACTAGT	ATGTAGAGAA
				TTGCACAAAT	TTATACTACT
601	GGGAGTCTGG	CCAAGGAAAA	GACACAGACC		
651	TTTTGCTGTA	TTTGATGAAG	GGAAAAGTTG	GCACTCAGAA	ACAAAGAACT
701	CCTTGATGCA	GGATAGGGAT	GCTGCATCTG	CTCGGGCCTG	GCCTAAAATG
751	CACACAGTCA	ATGGTTATGT	AAACAGGTCT	CTGCCAGGTC	TGATTGGATG
801	CCACAGGAAA	TCAGTCTATT	GGCATGTGAT	TGGAATGGGC	ACCACTCCTG
851	AAGTGCACTC	AATATTCCTC	GAAGGTCACA	CATTTCTTGT	GAGGAACCAT
901	CGCCAGGCGT	CCTTGGAAAT	CTCGCCAATA	ACTTTCCTTA	CTGCTCAAAC
951	ACTCTTGATG	GACCTTGGAC	AGTTTCTACT	GTTTTGTCAT	ATCTCTTCCC
			GCTTATGTCA	AAGTAGACAG	CTGTCCAGAG
1001	ACCAACATGA	TGGCATGGAA			
1051	GAACCCCAAC		AAATAATGAA	GAAGCGGAAG	ACTATGATGA
1101	TGATCTTACT	GATTCTGAAA	TGGATGTGGT	CAGGTTTGAT	GATGACAACT
1151	CTCCTTCCTT	TATCCAAATT		CCAAGAAGCA	TCCTAAAACT
1201	TGGGTACATT	ACATTGCTGC	TGAAGAGGAG	GACTGGGACT	ATGCTCCCTT
1251	AGTCCTCGCC	CCCGATGACA	GAAGTTATAA	AAGTCAATAT	TTGAACAATG
1301	GCCCTCAGCG	GATTGGTAGG	AAGTACAAAA	AAGTCCGATT	TATGGCATAC
1351	ACAGATGAAA	CCTTTAAGAC	GCGTGAAGCT	ATTCAGCATG	AATCAGGAAT
1401	CTTGGGACCT	TTACTTTATG	GGGAAGTTGG	AGACACACTG	TTGATTATAT
	_	AGCAAGCAGA	CCATATAACA	TCTACCCTCA	CGGAATCACT
1451	TTAAGAATCA				
1501	GATGTCCGTC	CTTTGTATTC	AAGGAGATTA	CCAAAAGGTG	TAAAACATTT
1551	GAAGGATTTT	CCAATTCTGC	CAGGAGAAAT	ATTCAAATAT	AAATGGACAG
1601	TGACTGTAGA	AGATGGGCCA		ATCCGCGGTG	CCTGACCCGC
1651	TATTACTCTA	GTTTCGTTAA	TATGGAGAGA	GATCTAGCTT	CAGGACTCAT
1701	TGGCCCTCTC	CTCATCTGCT	ACAAAGAATC	TGTAGATCAA	AGAGGAAACC
1751	AGATAATGTC	AGACAAGAGG	AATGTCATCC	TGTTTTCTGT	ATTTGATGAG
1801	AACCGAAGCT	GGTACCTCAC	AGAGAATATA	CAACGCTTTC	TCCCCAATCC
1851	AGCTGGAGTG		ATCCAGAGTT	CCAAGCCTCC	AACATCATGC
		TGGCTATGTT		TGCAGTTGTC	- ~~~~~~
1901		CATACTGGTA	CATTCTAAGC	ATTGGAGCAC	AGACTGACTT
1951	CATGAGGTGG				
2001	CCTTTCTGTC	TTCTTCTCTG	GATATACCTT	CAAACACAAA	
2051		CACCCTATTC	CCATTCTCAG	GAGAAACTGT	
2100	ATGGAAAACC			TGCCACAACT	CAGACTTTCG
2151	GAACAGAGGC	ATGACCGCCT	TACTGAAGGT	TTCTAGTTGT	GACAAGAACA
2201	CTGGTGATTA	TTACGAGGAC	AGTTATGAAG	ATATTTCAGC	ATACTTGCTG
2251		ATGCCATTGA	ACCTAGGAGC	TTCTCTCAGA	
2301	CTTGAAACGC		AAATAACTCG	TACTACTCTT	CAGTCAGATC
2351	AAGAGGAAAT		GATACCATAT	CAGTTGAAAT	
2401	$\nabla \lambda$ THOMOTOURY (1)	TTTATGATGA		CAGAGCCCCC	
740T	GATITIGACA	IIIAIGAIGA	GOVIGWWWI	CAGAGCCCCC	CCAGCIIICA

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3401 GGATGAGCAC ACTTTTTCTG GTGTACAGCA ATAAGTGTCA GACTCCCCTG 3451 GGAATGGCTT CTGGACACAT TAGAGATTTT CAGATTACAG CTTCAGGACA 3501 ATATGGACAG TGGGCCCCAA AGCTGGCCAG ACTTCATTAT TCCGGATCAA 3551 TCAATGCCTG GAGCACCAAG GAGCCCTTTT CTTGGATCAA GGTGGATCTG 3601 TTGGCACCAA TGATTATTCA CGGCATCAAG ACCCAGGGTG CCCGTCAGAA 3651 GTTCTCCAGC CTCTACATCT CTCAGTTTAT CATCATGTAT AGTCTTGATG 3701 GGAAGAAGTG GCAGACTTAT CGAGGAAATT CCACTGGAAC CTTAATGGTC	3401 GGATGAGCAC ACTTTTTCTG GTGTACAGCA ATAAGTGTCA GACTCCCCTG 3451 GGAATGGCTT CTGGACACAT TAGAGATTTT CAGATTACAG CTTCAGGACA 3501 ATATGGACAG TGGGCCCCAA AGCTGGCCAG ACTTCATTAT TCCGGATCAA 3551 TCAATGCCTG GAGCACCAAG GAGCCCTTTT CTTGGATCAA GGTGGATCTG 3601 TTGGCACCAA TGATTATTCA CGGCATCAAG ACCCAGGGTG CCCGTCAGAA 3651 GTTCTCCAGC CTCTACATCT CTCAGTTTAT CATCATGTAT AGTCTTGATG 3701 GGAAGAAGTG GCAGACTTAT CGAGGAAATT CCACTGGAAC CTTAATGGTC 3751 TTCTTTGGCA ATGTGGATTC ATCTGGGATA AAACACAATA TTTTTAACCC 3801 TCCAATTATT GCTCGATACA TCCGTTTGCA CCCAACTCAT TATAGCATTC 3851 GCAGCACTCT TCGCATGGAT TTGATGGGCT GTGATTTAAA TAGTTGCAGC 3901 ATGCCATTGG GAATGGAGG TAAAGCAATA TCAGATGCAC AGATTACTGC 3951 TTCATCCTAC TTTACCAATA TGTTTGCCAC CTGGTCTCCT TCAAAAGCTC	2451 2501 2551 2601 2651 2751 2801 2851 2951 3051 3151 3251 3301	AAAGAAAACA ATGGGATGAG AGTGTCCCTC CTTTACTCAG TGGGGCCATA AGAAATCAGG TGAGGAAGAT CTAATGAAAC ACTAAAGATG CCTGGAAAAA ACACTAACAC TTTGCTCTGT TGAAAATATG ATCCCACTTT ATGGATACAC GTATCTGCTC GTGGACATGT TACAATCTCT	CGACACTATT TAGCTCCCA AGTTCAAGAA CCCTTATACC TATAAGAGCA CCTCTCGTCC CAGAGGCAAG CAAAACTTAC AGTTTGACTG GATGTGCACT TTTTCACCAT GAAAGAAACT TAAAGAGAAT TACCTGGCTT AGCATGGCAT AGCATGGCA GTTCACTGTA ATCCAGGTGT	TTATTGCTGC CATGTTCTAA AGTTGTTTTC GTGGAGAACT GAAGTTGAAG CTATTCCTTC GAGCAGAACC TTTTGGAAAG CAAAGCCTGG CAGGCCTGAT GCTCATGGGA CTTTGATGAG GCAGGGCTCC TATCGCTTCC AGTAATGGCT GCAATGAAAA CGAAAAAAAG TTTTGAGACA	AGTGGAGAGG GAAACAGGGC CAGGAATTTA AAATGAACAT ATAATATCAT TATTCTAGCC TAGAAAAAAC TGCAACATCA GCTTATTTCT TGGACCCCTT GACAAGTGAC ACCAAAAGCT CTGCAATATC ATGCAATCAA CAGGATCAAA CATCCATTCT AGGAGTATAA GTGGAAATGT	CTCTGGGATT TCAGAGTGGC CTGATGGCTC TTGGGACTCC GGTAACTTTC TTATTTCTTA TTTGTCAAGC TATGGCACCC CTGATGTTGA CTGGTCTGCC AGTACAGGAA GGTACTTCAC CAGATGGAAG TGGCTACATA GGATTCGATG ATTCATTCA AATGGCACTG TACCATA
3601 TTGGCACCAA TGATTATTCA CGGCATCAAG ACCCAGGGTG CCCGTCAGAA 3651 GTTCTCCAGC CTCTACATCT CTCAGTTTAT CATCATGTAT AGTCTTGATG 3701 GGAAGAAGTG GCAGACTTAT CGAGGAAATT CCACTGGAAC CTTAATGGTC	3601 TTGGCACCAA TGATTATTCA CGGCATCAAG ACCCAGGGTG CCCGTCAGAA 3651 GTTCTCCAGC CTCTACATCT CTCAGTTTAT CATCATGTAT AGTCTTGATG 3701 GGAAGAAGTG GCAGACTTAT CGAGGAAATT CCACTGGAAC CTTAATGGTC 3751 TTCTTTGGCA ATGTGGATTC ATCTGGGATA AAACACAATA TTTTTAACCC 3801 TCCAATTATT GCTCGATACA TCCGTTTGCA CCCAACTCAT TATAGCATTC 3851 GCAGCACTCT TCGCATGGAT TTGATGGGCT GTGATTTAAA TAGTTGCAGC 3901 ATGCCATTGG GAATGGAGG TAAAGCAATA TCAGATGCAC AGATTACTGC 3951 TTCATCCTAC TTTACCAATA TGTTTGCCAC CTGGTCTCCT TCAAAAAGCTC	3351 3401 3451 3501	AGCTGGAATT GGATGAGCAC GGAATGGCTT ATATGGACAG	TGGCGGGTGG ACTTTTTCTG CTGGACACAT TGGGCCCCAA	AATGCCTTAT GTGTACAGCA TAGAGATTTT AGCTGGCCAG	TGGCGAGCAT ATAAGTGTCA CAGATTACAG ACTTCATTAT	CTACATGCTG GACTCCCCTG CTTCAGGACA TCCGGATCAA
	3801 TCCAATTATT GCTCGATACA TCCGTTTGCA CCCAACTCAT TATAGCATTC 3851 GCAGCACTCT TCGCATGGAT TTGATGGGCT GTGATTTAAA TAGTTGCAGC 3901 ATGCCATTGG GAATGGAGAG TAAAGCAATA TCAGATGCAC AGATTACTGC 3951 TTCATCCTAC TTTACCAATA TGTTTGCCAC CTGGTCTCCT TCAAAAGCTC	3601 3651 3701	TTGGCACCAA GTTCTCCAGC GGAAGAAGTG	TGATTATTCA CTCTACATCT GCAGACTTAT	CGGCATCAAG CTCAGTTTAT CGAGGAAATT	ACCCAGGGTG CATCATGTAT CCACTGGAAC	CCCGTCAGAA AGTCTTGATG CTTAATGGTC
4001 GACTTCACCT CCAAGGGAGG AGTAATGCCT GGAGACCTCA GGTGAATAAT 4051 CCAAAAGAGT GGCTGCAAGT GGACTTCCAG AAGACAATGA AAGTCACAGG 4101 AGTAACTACT CAGGGAGTAA AATCTCTGCT TACCAGCATG TATGTGAAGG 4151 AGTTCCTCAT CTCCAGCAGT CAAGATGGCC ATCAGTGGAC TCTCTTTTTT 4201 CAGAATGGCA AAGTAAAGGT TTTTCAGGGA AATCAAGACT CCTTCACACC 4251 TGTGGTGAAC TCTCTAGACC CACCGTTACT GACTCGCTAC CTTCGAATTC 4301 ACCCCCAGAG TTGGGTGCAC CAGATTGCCC TGAGGATGGA GGTTCTGGGC		4301	TGCGAGGCAC	AGGACCTCTA	C	ADDIADDADI	7505171155

FIG. 11B

Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

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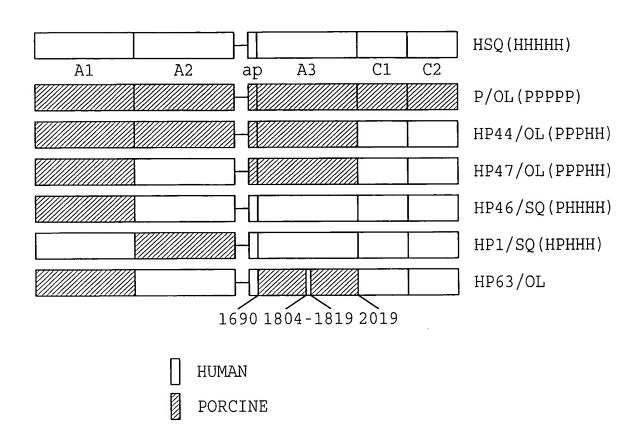


FIG. 12

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## AMINO ACID SEQUENCE OF HP63OL

1 51	MQLELSTCVF PATAPGALPL	LCLLPLGFSA GPSVLYKKTV	IRRYYLGAVE FVEFTDQLFS	LSWDYRQSEL VARPRPPWMG	LRELHVDTRF LLGPTIQAEV
101 151	YDTVVVTLKN GKSQTYVWQV	MASHPVSLHA LKENGPTASD	VGVSFWKSSE PPCLTYSYLS	GAEYEDHTSQ HVDLVKDLNS	REKEDDKVLP GLIGALLVCR
201 251	EGSLTRERTQ MHTVNGYVNR	NLHEFVLLFA SLPGLIGCHK	VFDEGKSWHS KSVYWHVIGM	ARNDSWTRAM GTSPEVHSIF	DPAPARAQPA LEGHTFLVRH
301	HRQASLEISP	LTFLTAOTFL	MDLGQFLLFC	HISSHHHGGM	EAHVRVESCA
351	EEPQLRRKAD	EEEDYDDNLY	DSDMÕVVRLD	GDDVSPFIQI	RSVAKKHPKT
401	WVHYIAAEEE	DWDYAPLVLA	PDDRSYKSQY	LNNGPQRIGR	KYKKVRFMAY
451	TDETFKTREA	IQHESGILGP	LLYGEVGDTL	LIIFKNQASR	PYNIYPHGIT
501	DVRPLYSRRL	PKGVKHLKDF	PILPGEIFKY	KWTVTVEDGP	TKSDPRCLTR
551	YYSSFVNMER	DLASGLIGPL	LICYKESVDQ	RGNOIMSDKR	NVILFSVFDE FDSLQLSVCL
601 651	NRSWYLTENI HEVAYWYILS	QRFLPNPAGV IGAQTDFLSV	QLEDPEFQAS FFSGYTFKHK	NIMHSINGYV MVYEDTLTLF	PFSGETVFMS
701	MENPGLWILG	CHNSDFRNRG	MTALLKVSSC	DKNTGDYYED	SYEDISAYLL
751 751	SKNNAIEPRS	FSONSRHPST	RSQNPPVLKR	HOREITRTTL	QSDQEEIDYD
801	DTISVEMKKE	DFÕIYDEDEN	QSPRSFQKRT	RĤYFIAAVEQ	<u> </u>
851	RALRNRAQNG	EVPRFKKVVF	REFADGSFTQ	PSYRGELNKH	LGLLGPYIRA
901	EVEDNIMVTF	KNQASRPYSF	YSSLISYPDD	QEQGAEPRKN	FVKPNETKTY
951	FWKVQHHMAP	TEDEFDCKAW	AYFSDVDLEK	DVHSGLIGPL	LICRANTLNA
1001	AHGROVTVOE	FALFFTIFDE	TKSWYFTENV	ERNCRAPCHL	QMEDPTLKEN
1051 1101	YRFHAINGYV RKKEEYKMAV	MDTLPGLVMA YNLYPGVFET	QNQRIRWYLL VEMLPSKVGI	SMGSNENIHS WRNRCLIGEH	IHFSGHVFSV LQAGMSTTFL
1151	VYSKKCQTPL	GMASGHIRDF	QITASGQYGQ	WAPKLARLHY	SGSINAWSTK
1201	EPFSWIKVDL	LAPMIIHGIK	ŤOGAROŘFSŠ	LYISQFIIMY	SLDGKKWQTY
1251	RGNSTGTLMV	FFGNVDSSGI	KĤNIFÑPPII	ARYIRLHPTH	YSIRSTLRME
1301	LMGCDLNSCS	MPLGMESKAI	SDAQITASSY	FTNMFATWSP	SKARLHLQGR
1351	SNAWRPQVNN	PKEWLQVDFQ	KTMKVTGVTT	QGVKSLLTSM	YVKEFLIŠSS
1401	QDGHQWTLFF	QNGKVKVFQG	NQDSFTPVVN	SLDPPLLTRY	LRIHPQSWVH
1451	QIALRMEVLG	CEAQDLY			

FIG. 13

Title: Nucleic Acid and Amino Acid Sequences Encoding High-Level

Expressor Factor VIII Polypeptides and Methods of Use

Inventor(s): Lollar

Application No: To be Assigned Atty Dkt No: 007157/276516

#### 32/33

#### NUCLEOTIDE SEQUENCE OF HP63/OL

```
TGCCACTCGG
                  AGCTCTCCAC
                              CTGTGTCTTT
                                          CTGTGTCTCT
      ATGCAGCTAG
                                                       CTGTCCTGGG
      CTTTAGTGCC
                              ACTACCTGGG
                                          CGCAGTGGAA
 51
                  ATCAGGAGAT
                              CTCCGTGAGC
TCTTCCGTTG
101
      ACTACCGGCA
                  AAGTGAACTC
                                          TGCACGTGGA
                                                       CACCAGATTT
                                                       TCCTGTACAA
                                          GGCCCGTCAG
                  CGCCAGGAGC
151
      CCTGCTACAG
                                          ACTTTTCAGC
                                                       GTTGCCAGGC
                              TCACGGATCA
      AAAGACTGTG
                  TTCGTAGAGT
201
                                                       GGCTGAGGTT
                              CTGCTGGGTC
                                          CTACCATCCA
251
      CCAGGCCACC
                  ATGGATGGGT
                                                       ATCCCGTTAG
301
      TACGACACGG
                  TGGTCGTTAC
                              CCTGAAGAAC
                                          ATGGCTTCTC
      TCTTCACGCT
                              CCTTCTGGAA
                                          ATCTTCCGAA
                                                       GGCGCTGAAT
                  GTCGGCGTCT
351
                                          AAGACGATAA
                                                       AGTCCTTCCC
                              AGGGAGAAGG
                  CACCAGCCAA
401
      ATGAGGATCA
                                                       ATGGTCCAAC
                              CTGGCAGGTC
                                          CTGAAAGAAA
451
      GGTAAAAGCC
                  AAACCTACGT
                                          ATACCTGTCT
                                                       CACGTGGACC
                              TTACCTACTC
501
      AGCCTCTGAC
                  CCACCATGTC
                                          GAGCCCTGCT
                                                       GGTTTGTAGA
551
      TGGTGAAAGA
                  CCTGAATTCG
                              GGCCTCATTG
                              AAGGACCCAG
                                          AACCTGCACG
601
      GAAGGGAGTC
                  TGACCAGAGA
                                                       AATTTGTACT
                                           TTGGCACTCA
CTGCCAGGGC
      ACTTTTTGCT
                  GTCTTTGATG
                              AAGGGAAAAG
                                                       GCAAGAAATG
651
                                                       CCAGCCTGCA
701
      ACTCCTGGAC
                  ACGGGCCATG
                              GATCCCGCAC
                                           TCTCTGCCAG
                                                       GTCTGATCGG
                  TCAATGGCTA
                              TGTCAACAGG
      ATGCACACAG
751
                                           GATTGGAATG
                                                       GGCACCAGCC
      ATGTCATAAG
                  AAATCAGTCT
                              ACTGGCACGT
801
851
                  CTCCATTTTT
                              CTTGAAGGCC
                                           ACACGTTTCT
                                                       CGTGAGGCAC
      CGGAAGTGCA
                  CTTCCTTGGA
                              GATCTCGCCA
                                           CTAACTTTCC
                                                       TCACTGCTCA
901
      CATCGCCAGG
                  ATGGACCTTG
                              GCCAGTTCCT
                                          ACTGTTTTGT
                                                       CATATCTCTT
      GACATTCCTG
 951
                                                       AAGCTGCGCC
                              GAGGCTCACG
                                           TCAGAGTAGA
1001
      CCCACCACCA
                  TGGTGGCATG
                                           GAAGAGGAAG
                                                       ATTATGATGA
                              GAAAGCTGAT
1051
      GAGGAGCCCC
                  AGCTGCGGAG
                                           CCGGCTCGAT
                                                       GGTGACGACG
1101
      CAATTTGTAC
                  GACTCGGACA
                               TGGACGTGGT
      TGTCTCCCTT
                               CGCTCAGTTG
                                           CCAAGAAGCA
                                                       TCCTAAAACT
                  TATCCAAATC
1151
                  ACATTGCTGC
                                           GACTGGGACT
                                                       ATGCTCCCTT
1201
      TGGGTACATT
                               TGAAGAGGAG
                                           AAGTCAATAT
                                                       TTGAACAATG
      AGTCCTCGCC
                  CCCGATGACA
                              GAAGTTATAA
1251
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                                           AAGTCCGATT
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      GCCCTCAGCG
                  GATTGGTAGG
1301
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                                           ATTCAGCATG
                                                       AATCAGGAAT
      ACAGATGAAA
                  CCTTTAAGAC
1351
                  TTACTTTATG
                               GGGAAGTTGG
                                           AGACACACTG
                                                       TTGATTATAT
      CTTGGGACCT
1401
                               CCATATAACA
                                           TCTACCCTCA
                                                       CGGAATCACT
1451
                  AGCAAGCAGA
      TTAAGAATCA
                                                       TAAAACATTT
                              AAGGAGATTA
                                           CCAAAAGGTG
1501
      GATGTCCGTC
                  CTTTGTATTC
                                           ATTCAAATAT
                                                       AAATGGACAG
      GAAGGATTTT
                               CAGGAGAAAT
1551
                  CCAATTCTGC
                                                       CCTGACCCGC
                                           ATCCTCGGTG
                              ACTAAATCAG
1601
      TGACTGTAGA
                  AGATGGGCCA
      TATTACTCTA
TGGCCCTCTC
                                           GATCTAGCTT
                                                       CAGGACTCAT
                  GTTTCGTTAA
                               TATGGAGAGA
1651
                  CTCATCTGCT
                                           TGTAGATCAA
                                                       AGAGGAAACC
                               ACAAAGAATC
1701
                               AATGTCATCC
                                           TGTTTTCTGT
                                                       ATTTGATGAG
1751
      AGATAATGTC
                  AGACAAGAGG
                                           CAACGCTTTC
                                                       TCCCCAATCC
      AACCGAAGCT
                  GGTACCTCAC
                               AGAGAATATA
1801
                                           CCAAGCCTCC
                                                       AACATCATGC
                               ATCCAGAGTT
1851
      AGCTGGAGTG
                  CAGCTTGAGG
                                                       AGTTTGTTTG
1901
                  TGGCTATGTT
                               TTTGATAGTT
                                           TGCAGTTGTC
      ACAGCATCAA
      CATGAGGTGG
                   CATACTGGTA
                               CATTCTAAGC
                                           ATTGGAGCAC
                                                       AGACTGACTT
1951
                  TTCTTCTCTG
                               GATATACCTT
                                           CAAACACAAA
                                                       ATGGTCTATG
      CCTTTCTGTC
2001
                                           GAGAAACTGT
                               CCATTCTCAG
                                                       CTTCATGTCG
      AAGACACACT
                   CACCCTATTC
2051
                                                       CAGACTTTCG
                               GATTCTGGGG
                                           TGCCACAACT
                   CAGGTCTATG
2101
      ATGGAAAACC
                                                       GACAAGAACA
      GAACAGAGGC
                  ATGACCGCCT
                                           TTCTAGTTGT
                               TACTGAAGGT
2151
                                                       ATACTTGCTG
                   TTACGAGGAC
                               AGTTATGAAG
                                           ATATTTCAGC
2201
      CTGGTGATTA
                  ATGCCATTGA
                               ACCTAGGAGC
                                                       ATTCAAGACA
                                           TTCTCCCAGA
2251
      AGTAAAAAACA
                  AGGTCTCAAA
                               ACCCACCAGT
                                           CTTGAAACGC
                                                       CATCAACGGG
2301
      CCCTAGCACT
                                          AAGAGGAAAT
                                                       TGACTATGAT
                  TACTACTCTT
                              CAGTCAGATC
2351
      AAATAACTCG
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FIG. 14B